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(without alignments)
697.011 Million cell updates/sec
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1 MTSGEVKTSLKNAYSSAKRL......VQQRRRSQRQDGEEEDGREL 220
                                                                                                                                                                  8, 2002, 15:38:16; Search time 23.38 Seconds
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| SIDSB/gcgdata/geneseqg/geneseqp/AA1981.DAT:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      522463 seqs, 74073290 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                   Title:
Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:\*/SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:\*

/SIDS8/gcgdata/geneseq/geneseqp/AA1997 .DAT: /SIDS8/gcgdata/geneseq/geneseqp/AA1998 .DAT: /SIDS8/gcgdata/geneseq/geneseqp/AA1999 .DAT:

## SUMMARIES

,		Description	Human SGP003 phosp	A human regulator	Human phosphatase	Amino acid sequenc	Human ORFX ORF2098	Human cardiovascul	Murine phosphatase	Human polypeptide	Human DSP-7. Homo	Human dual specifi	Human polypeptide
		OI .	-	AAB18667	AAB73219	AAY68779	AAB42334	AAY92177	AAB73214	AAM39977	AAB28519	AAY85620	AAM39356
		: BB	22	21	22	21	21	21	22	22	21	21	22
		Match Length DB ]	220	221	198	248	318	221	198	327	291	211	211
æ	Query	Match	99.8	88.4	40.1	40.1	40.1	39.9	39.7	39.7	39.3	38.3	38.3
	,	Score	1159	1026.5	465.5	465.5	465.5	463.5	461	460.5	456.5	445	445
	Result	٠ ا	1	7	æ	4	S	ø	7	60	σ	10	11

/note= "Encoded by CTG"

WO200146394-A2

Human SGP060 phosp Human polypeptide Human SGP014 phosp Human hydrolase-11 Human SGP018 phosp Human cardlovascul			Human JNK activati Anino acid sequenc Human phosphatase Human Gal-specifi Human DSP-3 protei Murine phosphatase Murine DSP-3 varia	
AAE04839 AAM42355 AAE04838 AAB28793 AAE04836 AAY92175	AAE0678 AAB6644 AAR5696 AAW3533 AAB4287		AABB1105 AAX68795 AAB77216 AAB67167 AAB66431 AAB7333 AAB66443	
		250 251 276 222 240 21 167 21 173 222		179 22 80 22 169 22 169 22 302 22 392 18 394 15
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12 13 14 15 16	118 220 222	22 2 2 2 4 2 2 4 3 3 4 4 3 4 4 3 4 4 4 4		# C 2/10 Dafts

## ALIGNMENTS

.DAT:

/SIDS8/gcgdata/geneseq/geneseqp/AA1989

/SIDSB/gcgdata/geneseq/geneseqp/AA1990.DAT. /SIDSB/gcgdata/geneseq/geneseqp/AA1991.DAT. /SIDSB/gcgdata/geneseqy/geneseqp/AA1992.DAT. /SIDSB/gcgdata/geneseqy/geneseqp/AA1993.DAT. /SIDSB/gcgdata/geneseqy/geneseqp/AA1993.DAT. /SIDSB/gcgdata/geneseqy/geneseqp/AA1994.DAT. /SIDSB/gcgdata/geneseqy/geneseqp/AA1996.DAT.

Parkinson's disease; multiple sclerosis; amyorrophic lateral sclerosis; cardiovascular disease; brain; neuronal-associated disease; dyskinesia; attention disorder; copition disorder; psychotic disorder; dyostatic; neurological disorder; virucide; nootropic; cerebroprotective; therapy; neuroprotective; antibacterial; vulnerary; tranquilliser; antiasthmatic; hyptensive; immuosuppressive; antipsoriatic; analgesic; hypertensive; antifungal; dual specificity phosphatase; DSP; MAP kinase phosphatase; MKP; migraine; chromosome CHR10. Human; SGP003 phosphatase polypeptide; phosphatase-related disease; immune-related disorder; ocular disease; organ transplant rejection; infection; diabetes; pain; sexual dysfunction; Alzheimer's disease; metabolic disorder; haematopoletic cancer; mood disorder; cardiant; Domain /label - Catalytic\_domain 54..199 /label - Phosphatase\_domain Misc-difference 85 Human SGP003 phosphatase polypeptide. Location/Qualifiers AAE04837 standard; Protein; 220 AA (first entry) Homo sapiens. 10-SEP-2001 AAE04837; Key Domain AAE04837 RESULT 

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The present invention relates to phosphatase polypeptides, nucleotide sequences encoding them, as well as various products and methods useful for the diagnosis and treatment of various phosphatase-related diseases and conditions. Substance that modulates the activity of phosphatase polypeptide is used to treat immune-related diseases and disorders, cardiovascular disease, brain or neuronal associated diseases and metabolic disorders, including cancers of tissues, cancers of hematopoletic origin, diseases of central and peripheral nervous system, Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, viral infections, infections caused by prions bacteria and fungi, ocular diseases, diabetes, migraines, pain, sexual dysfunction, mood disorders, attention disorders, neurological disorders, hypotension, hypertension, psychotic disorders, neurological disorders, dyskinesias and organ transplant rejection. The present amino acid sequence is human Scp003 phosphatase polypeptide. This sequence is classified as dual specificity phosphatase (DSP) and MAP curion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                   Novel phosphatase polypeptide useful for treating cancers, immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases and metabolic disorders
                                                                                                                                                                                           Hill RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 LSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKN 180
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1; Mismatches
                                                                                                                                                                                           Whyte D,
                                                                                                                                                                                                                                                                                                                                                     Claim 7; Fig 2; 186pp; English.
                                                                            99US-0173255.
99US-0175766.
2000US-0178078.
                                              21-DEC-2000; 2000WO-US34736
                                                                                                                          2000US-0179301
                                                                                                                                                                                         Plowman GD, Martinez R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 99.5
nes 219; Conservative
                                                                                                                                                                                                                                      WPI; 2001-418058/44.
N-PSDB; AAD09495.
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                                                                                                                                                           (SUGE-) SUGEN INC.
                                                                                              28-DEC-1999;
25-JAN-2000;
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                                                                             21-DEC-1999:
                28-JUN-2001
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AAB18667 standard; Protein; 221

AAB18667

AAB18667

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The present sequence represents a human regulator of intracellular phosphorylation (HRIP). HRIP is useful for screening agonists and antagonists of HRIP polypeptide. HRIP and its agonist or antagonist are useful for treating a disease or condition associated with decreased or increased expression of functional HRIP. Diseases treated or diagnosed include neurological disorders such as stroke, Parkinson's disease, demyelinating diseases, bacterial and viral meningitis and neuromnscular disorders, myasthenia gravis, cell proliferative disorders such as actinic Keratosis, anteriosclerosis, atherosclerosis and cancer including leukaemia, melanoma, myeloma and cancer of the adrenal gland, bladder, bone marrow, liver, lung, muscle, ovary, autoimmune/ inflammatory disorders such as Addison's disease, acquired immunodeficiency diseases, allergies, bronchitis, diabetes mellitus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human intracellular phosphorylation regulator polypeptides and polynucleotides for diagnosis, prevention and treatment of neurological, cell proliferative and autoimmune/inflammatory disorders
                                                                    stroke; myeloma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "tyrosine specific protein phosphatase active
                                                               Human; intracellular phosphorylation regulator; HRIP; stroke; myelon neurotogical disorder; Parkinson's disease; demyelinating disease; meningitis; developmental disorder; neuromuscular disorder; cancer; myasthenia gravis; cell proliferative disorder; actinic keratosis;
                                                                                                                                  arteriosclerosis; atherosclerosis; leukaemia; melanoma; bronchitis; autofimune disorder; inflammatory disorder; Addison's disease; acquired immunodeficiency disease; allergy; diabetes mellitus; rheumatoid arthritis; microbial infection; trauma.
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                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "potential phosphorylation site"
170
                                                                                                                                                                                                                                                                                     /note= "potential phosphorylation site"
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208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "potential phosphorylation site"
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                              A human regulator of intracellular phosphorylation.
                                                                                                                                                                                                                                                Location/Qualifiers
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99US-0135049.
99US-0143188.
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22-JAN-2001 (first entry)
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146..158
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09-JUL-1999;
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Local Similarity
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03-NOV-1998;
19-NOV-1998;
22-DEC-1998;
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14-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phosphatase; gene therapy; enzyme; cancer; pathophysiological hypoxia; cardiac dysfunction; vascular disorder; myopathy; ectodermal dysplasia; congenital muscle disorder; Papillon-Lefevre syndrome; Cowden disease; Moebius, syndrome; Bjornstad syndrome; Bannayan Zonama syndrome;
                                                                                                                                                                                                                                         ppfdlsvffypaaafidralsddhskilvhcvmgrsrsatlvlaylmihkdmtlvdaigg 177
                                                                                                                                                                                                                          KLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDLPT-- 118
                                                                                                                                                                                                                                                                              --FDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQ 176
                                                                                                                                          Gaps
                                                                                                                                                                                  New protein phosphatase polypeptide for diagnosing and treating phosphatase related disorders such as cancer, schizophrenia, cardiac dysfunction and/or vascular disorders
                                                                                                                                                                    1 MTSGEVKTSLKNAYSSAKRLSPKMEEEGEEEDYCTPGAFELERLFWKGSPQYTHVNEVWP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention relates to phosphatase proteins and coding
                                                                                                               Length 221;
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                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                    VAKNRCVLPNRGFLKQLRELDKQLVQQRRRSQRQDGEEEDGREL 220
                                                                                                                                                                                                                                                                                                                                                 rheumatoid arthritis, microbial infection and trauma.
                                                                                                               DB 21;
                                                                                                                          Pred. No. 4.4e-112;
1; Mismatches 12;
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                                                                                                                Score 1026.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                AAB73219 standard; Protein; 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human phosphatase LOC51207_h.
                                                                                                               Query Match 88.4%;
Best Local Similarity 91.1%;
Matches 204; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    schizophrenia; hamartoma
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                                                                       221 AA;
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                                                                       Sequence
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ID AAB7
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glioblastoma, colorectal cancer and thyroid cancer, pathophysiological hypoxia, cardiac dysfunction and/or vascular disorders, myopathies, congenital muscle disorders, Papillon-Lefevre syndrome, Cowden disease, ectodermal dysplasia, Moebius syndrome, Bjornstad syndrome, Bannayan Zonana syndrome, schizophrenia and hamartomas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                  PKMEEEGEEEDYCTPGAFELERLFW-KGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAG 80
                                                                                                                                                                                                                                                                                                                            site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of a human phosphorylation effector PHSP-11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phosphorylation effector; PHSP; proliferative disorder; disorder; neuronal disorder.
                                                                                                                                                                                                              Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "tyrosine specific phosphatase active
                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note- "potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "potential glycosylation site"
                                                                                                                                                                                                              DB 22;
                                                                                                                                                                                                           40.1%; Score 465.5; DB 2
48.9%; Pred. No. 2.6e-46;
iive 36; Mismatches 58
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98US-0152814.
98US-0173482.
98US-0106889.
98US-0109093.
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                                                                                                                                                                                                                                                        Conservative
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245
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allergy;
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Oy
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                                                                                                                                                                                                                                                                                                          (PHSP), designated PHSP1-PHSP31 (the protein sequence for PHSP28 is not yearen in the specification). The sequences were isolated from CDNA libraries prepared from various human tissues. The PHSP proteins are useful for the diagnosis, treatment and prevention of proliferative disorders, immune disorders and neuronal disorders. The PHSP proteins form pharmaceutical compositions which useful for treating or preventing disorders associated with decreased PHSP expression/activity. PHSP antagonists are useful for treating or preventing disorders associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; antiantantic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coaqulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidifammatory; antianaemic; gene therapy; cancer; proliferative disorder; hypottension; antianaemic; gene therapy; cancer; proliferative disorder; hypotrension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
                                                                                                                                                                                                             treatment
                                                                                     Baughn MR;
H, Azimzai Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 FTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDH 140
                                                                                                                                                                                                                                                                                          AAY68769-95 and AAY68797-99 represent human phosphorylation effectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 PKMEEEGEEEDYCTPGAFELERLFW-KGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAG 80
                                                                                                                                                                                                      human phosphorylation effectors useful for the diagnosis, t
prevention of proliferative, immune and neuronal disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40.1%; Score 465.5; DB 21; Length 248; 48.9%; Pred. No. 3.7e-46; Live 36; Mismatches 58; Indels 1;
                                                                                    YT, Corley NC, Guegler KJ,
Au-Young J, Gorgone GA, Yue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human ORFX ORF2098 polypeptide sequence SEQ ID NO:4196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  with increased PHSP expression/activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB42334 standard; Protein; 318 AA.
                                                                                                                                                                                                                                                            Claim 1; Page 91; 142pp; English.
                                                                                  Lal P, Tang YT,
99US-0173482.
99US-0229005.
                                                                                                    Bandman O, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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Matches 91; Conservative
                                                  (INCY-) INCYTE PHARM INC.
                                                                                                                                                  WPI; 2000-183125/16.
                                                                                                                  Reddy R, Lu DAM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248 AA;
                                                                                                                                                                        N-PSDB; AAZ46148
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12-JAN-1999;
12-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-FEB-2001
                                                                                                  Patterson C,
                                                                                  Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; sequences have activities such as: cytostatic; hepatotropic; vulnerary; cytospathic; antiparkinsonian; nocircopic; neuroprotective; vulnerary; antiparkinsonian; nocircopic; immunosuppressant; limunostimulant; cardiant; thrombolytic; cytogulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; the presence of or predisposition to, or preventing or treatining the presence of or predisposition to, or preventing or treating the proteins and nucleic acids may be used to treat cancers; proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, dlabetes mellitus, cythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, auticimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antinifiammatory disease; to enhance companied immunodesis; and as a contraceptive.
allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 SKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 PKMEEEGEEEDYCTPGAFELERLFW-KGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAG
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48.9%; Pred. No. 5.3e-46;
ive 36; Mismatches 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Page 3392-3393; 5507pp; English
                                                                                                                                                                                                                                                                                                                                                                               2000WO-US08621
                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-602362/57.
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                                                                                                                                                                                                                            WO200058473-A2
                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000;
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                                                                                                                                                                                                                                                                                                      05-OCT-2000.
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Matches 9
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Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New cardiovascular system associated protein tyrosine phosphatases are used in the diagnosis and treatment of e.g. immune disorders, anti-proliferative disorders, metabolic disorders and cardiovascular
                                                                                                                                                                                                                                                       Human cardiovascular system associated protein tyrosine phosphatase 4.
                                                                                                                                                                                                                                                                                                   Cardiovascular system associated protein tyrosine phosphatase 4; CSAPTP-4; cytostatic; immunomodulatory; antidiabetic; virucide; hypotensive; cardiant; tyrosine phosphatase modulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218 .220
/note= "Protein Kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68.221
/note= "phosphatase catalytic active domain"
164.169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note- "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "N-glycosylation site"
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/label- N_terminal_domain
/note- "unique"
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                               AAY92177 standard; Protein; 221 AA.
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98US-0164193.
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                                                                                                                                                                                                           (first entry)
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312 gretgr 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
Domain
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to determine efficacy of a treatment procedure. CSAPTP nucleic acids, antibodies and protein molecules can be used in screening assays and in predictive medicine e.g. prognostic assays, monitoring clinical trials
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phosphatase; gene therapy; enzyme; cancer; pathophysiological hypoxia; cardiac dysfunction; wascular disorder; myopathy; ectodermal dysplasia; congenital muscle disorder; Papillon-Lefevre syndrome; Cowden disease; Moebius syndrome; Bjornstad syndrome; Bannayan Zonana syndrome; schizophrenia; hamartoma.
                                                                                                                                                                                                                                                                            FTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDH 140
                                                                                                                                                                                                                                                                                                                                               New protein phosphatase polypeptide for diagnosing and treating phosphatase related disorders such as cancer, schizophrenia, cardiac dysfunction and/or vascular disorders
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                                                                                                                                                                                                                                                                                                PKMEEEGEEEDYCTPGAFELERLFW-KGSPQYTHVNEVWPKLY IGDEATALDRYRLQKAG
                                                                                                                                                                                                                               Lioubin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention relates to phosphatase proteins and coding
                                                                                                                                                                          ä
                                                                                                                                        DB 21; Length 221;
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                                                                                                                                      39.9%; Score 463.5; DB 2
50.0%; Pred. No. 5.3e-46;
iive 34; Mismatches 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Fig 5; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine phosphatase AA144705_m.
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                                                                                                                                                        Local Similarity 50.0%
hes 90; Conservative
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                                                       and pharmacogenetics.
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                                                                                      221
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                                                                                       Sequence
                                                                                                                                         Query Match
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                                                                                                                                                                                               327
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25-MAY-1999;
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                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                   Best Loca
Matches
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                                                                                                                                                                                                                                                                                141
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AAB28519
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myopathies,
Cowden disease,
                                                                                                                                                                                                                                                                                                                                                               Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang D;
                                                                                                                                                 81 FTHVLNAAHGRWNVDTGPDYYRDMDIQYHCVEADDLPTFDLSVFFYPAAAFIDRALSDDH 140
                                                                                                                                                                                             Gaps
hypoxia, cardiac dysfunction and/or vascular disorders, myopathies, congenital muscle disorders, Papillon-Lefevre syndrome, Cowden disea. ectodermal dysplasia, Moebius syndrome, Bjornstad syndrome, Bannayan Zonana syndrome, schizophrenia and hamartomas.
                                                                                                              PKMEEEGEEEDYCTPGAFELERLFW-KGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAG 80
                                                                                                                        Novel nucleic acids and polypeptides, useful for treating disorders
                                                                                                                                                            SKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQL
                                                                                             4 ;
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Zhang J
                                                                         Length 198;
                                                                                           59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qian XB,
Yang Y,
                                                                        Score 461; DB 22;
Pred. No. 8.9e-46;
32; Mismatches 59;
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Xu C, Xue AJ,
,, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen R,
                                                                                                                                                                                                                                                                                        AAM39977 standard; Protein; 327 AA
                                                                                                                                                                                                                                                                                                                                               Human polypeptide SEQ ID NO 3122.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C, Asundi V, CP
Wang Z, Wehrman T, X
Zhou P, Goodrich R,
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2000US-0552317.
2000US-0598042.
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2000US-0653450.
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2000US-0693036
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                                                                                           94; Conservative
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N-PSDB; AAI59133.
                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                         201 VQQRRRSQR 209
                                                                                                                                                                                                                                           ---rretgr 197
                                              198 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-APR-2000;
09-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                               leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tang YT,
Wang J, V
Zhao QA,
                                                                                                                                                                                                                                                                                                          AAM39977;
                                               Sequence
                                                                                            Matches
                                                                                                             22
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in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries of the peripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and constants.
                                                                                                                                                The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDH 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261 grvlvhcamgvsrsatlvlaflmicenmtlveaiqtvqahrnicpnsgflrqlqvldnrl 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PKMEEEGEEEDYCTPGAFELERLFW-KGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.7%; Score 460.5; DB 2
48.9%; Pred. No. 2.1e-45;
iive 35; Mismatches 59
                                                                        Example 4; SEQ ID NO 3122; 10078pp; English
such as central nervous system injuries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB28519 standard; Protein; 291 AA
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99US-0135757
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99US-0128203

07-APR-1999;

(CEPT-) CEPTYR INC Wei

Luche RM,

WPI; 2000-656232/63. N-PSDB; AAC61100.

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isolation of dual-specificity mitogen-activated protein kinase (MAPK) phosphatase DSP-7. The antibody specific to DSP-7 and the antisense phosphatase DSP-7. The antibody specific to DSP-7 are useful for detecting DSP-7 expression in a sample which comprises an RNA or cDNA preparation. The antibody is linked to a support material and a detectable marker and the amount of DSP-7 polynucleotide hybridized to the antisense polynucleotide is determined using PCR or hybridisation assay. The isolated DSP-7 polypeptide is useful for screening agents that modulate DSP-7 activity. The identified agents are useful for treating Duchenne muscular dystrophy, cancer, graft-versus-host disease, autoimmune diseases, allergies, metabolic diseases, abnormal cell growth, abnormal cell proliferation and cell cycle abnormalities.
                                                                                                                  Novel dual-specificity mitogen-activated protein kinase phosphatase polypeptide used in assays to identify agents that modulate the enzyme's activity, which are useful for treating cancer and autoimmune diseases
                                                                                                                                                                                                                                                                                           present sequence is given in a method relating to the
                                                                                                                                                                                                                                         Claim 1; Fig 2A; 70pp; English.
                                                          WPI; 2000-679377/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           291 AA;
                     Wei B;
                                                                                        N-PSDB; AAC62749
                     Luche RM,
                                                                                                                                                                                                                                                                                        The
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Gaps DB 21; Length 291; Indels Score 456.5; DB 21; Pred. No. 5.3e-45; 6; Mismatches 59; 36; 39.3%; 48.4%; Conservative Local Similarity 90; Query Match Best Loc Matches

Sequence

1; 81 FTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDH 140 22 PKMEEEGEEEDYCTPGAFELERLFW-KGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAG 141 SKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQL 201 VQQRRR 206 gretgr 290 105 | g 셤 ò g ò ò 셤 ç

AAY85620 standard; Protein; 211 AA. 06-FEB-2001 (first entry) AAY85620; 

Human dual specificity phosphatase-9 (DSP-9) amino acid sequence.

Dual specificity phosphatase-9; DSP-9; human; cytostatic; cell growth; immunosuppressive; antiallergic; antiproliferative; autoimmune disease; cancer; graft-versus-host disease; allergy; metabolic disorder.

Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

Homo sapiens

leukaemia

WO200060100-A1 12-OCT-2000.

Homo sapiens

07-APR-2000; 2000WO-US09321.

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                                                                                                                                                                                                                                                                                   Included in the invention are an expression vector comprising a polynucleotide encoding the DSP-9 protein, a host cell transformed by the expression vector, and an antibody that specifically binds to DSP-9. DSP-9 has cytostatic; immunosuppressive; antiallargic; and antiprolliferative activity. DSP-9 modulating agents are useful for modulating a proliferative response, differentiation or survival of a cell which displays contacting inhibition of cell growth, anchorage independent growth or an altered intercellular adhesion property, in a patient. DSP-9 agonists and antiagonists are also useful for treating a disorder associated with DSP-9 activity such as Duchenne muscular dystrophy, cancer, graft-versus-host disease, autoimmune disease, allergies, metabolic disease, abnormal cell growth, abnormal cell cycle abnormalities. The present sequence
                                                                                                                                                                                                                                                                                                           the
                                                                                                                                    Dual specificity phosphatase-9 which dephosphorylates activated mitogen-activated protein kinase, used to identify agents that inhibit DSP-9 activity and modulate cell proliferation, differentiation, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to an isolated dual specificity phosphatase-9 (DSP-9) and its variant. The DSP-9 protein has the ability to dephosphorylate an activated mitogen activated protein (MAP) kinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FELERLFWKGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQLVQ 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.3%; Score 445; DB 21;
llarity 54.3%; Pred. No. 7.4e-44;
Conservative 26; Mismatches 47;
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                                                                                                                                                                                                             Claim i; Fig 2A; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
es 89; Conserv
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                                                                                                                                                                                    survival
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66
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us-09-847-519a-2.rag

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immune related disorder; ocular disease; organ transplant rejection;
infection; diabetes; pain; sexual dysfunction; Alzheimer's disease;
metabolic disorder; haematopoietic cancer; mood disorder; cardiant;
                                             SGP060 phosphatase polypeptide; phosphatase-related disease;
               Human SGP060 phosphatase polypeptide
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Best Local Similarity
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                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                       Homo
    The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system (iseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and constants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                   Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 FELERLFWKGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGP
                                                                                                                                                                                                                                                 Ren F, W
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38.3%; Score 445; DB 22; Length 211; 54.3%; Pred. No. 7.4e-44; ive 26; Mismatches 47; Indels ;
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Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159 LAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQLVQ 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen R, Ma Y,
Xu C, Xue AJ,
R, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE04839 standard; Protein; 211 AA
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Wehrman T, Xu
Goodrich R,
                                                                                                              20000S-0598042.
20000S-0620312.
20000S-0653450.
20000S-0662191.
20000S-06631036.
                                                      26-DEC-2000; 2000WO-US34263
                                                                                    2000US-0488725
2000US-0552317
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Best Local Similarity 54.33
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                      WPI; 2001-442253/47.
N-PSDB; AAI58512.
                                                                                                                                                                                                                                                Liu C,
Wang 2,
                                                                                                                                                                                                                                                                             Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 AA;
                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specification
                                                                                                                                                                       19-OCT-2000;
                                                                                                                                19-JUL-2000;
                                                                                                                                            03-AUG-2000;
                                                                                                                                                             14-SEP-2000;
                                                                                    21-JAN-2000;
25-APR-2000;
                                                                                                                 09-JUL-2000;
                            26-JUL-2001
                                                                                                                                                                                                                                                                             Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE04839;
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                                                                                                                                                                                                                                                Tang YT,
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The present invention relates to phosphatase polypeptides, nucleotide sequences encoding them, as well as various products and methods useful for the diagnosis and treatment of various phosphatase-related diseases and conditions. Substance that modulates the activity of phosphatase polypeptide is used to treat immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases and metabolic disorders, including cancers of tissues, cancers of hemmatopoietic origin, diseases of central and peripheral nervous system, Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, viral infections, infections caused by prions, bacteria and fungi, ocular diseases, diabetes, migraines, pain, sexual dysfunction, mood disorders, attention disorders, neurological disorders, hypotension, hypetension, psychotic disorders, neurological disorders, dyskinesias and organ transplant rejection. The present amine acid sequence is human Scp060 phosphatase (DSP) and MAP chinse phosphatase (MKP). SGP060 gene maps to chromosomal position
Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; cardiovascular disease; brain; neuronal-associated disease; dyskinesia; attention disorder; cognition disorder; psychotic disorder; cytostatic; neurological disorder; virucide; nootropic; cerebroprotective; therapy; neuroprotective; antibacterial; vulnerary; tranquilliser; antiasthmatic; hypotensive; immunosuppressive; antipsoriatic; analgesic; hypertensive; antifungal; dual specificity phosphatase; DSP; MAP kinase phosphatase; MRP; migraine; chromosome 8p11.1-q11.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel phosphatase polypeptide useful for treating cancers, immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases and metabolic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hill RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Martinez R, Whyte D, Manning G, Sudarsanam S,
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Pred. No. 7.4e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61..204
/label- Phosphatase_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Catalytic_domain 61..204
                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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54.3%;
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28-DEC-1999; 99US-0175766.
25-JAN-2000; 2000US-0178078.
31-JAN-2000; 2000US-0179301.
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N-PSDB; AAD09497.
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                                                                                                                                                                                                                                                                                                                                                                   sapiens
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Flanagan P;
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8p11.1-q11.1
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Claim 11;
           Rosen CA,
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                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                       Human: nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder;
                        DYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLV 158
                                                      Gaps
                                                                                                                                                                                                                                   neurological disease; infection; nephrotropic; gene therapy; vaccine
                 FELERLFWKGSPQYTHVNEVWPKLYIGDEATALDRYRLOKAGFTHVLNAAHGRWNVDTGP
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   47; Indels
                                                                           LAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQLVQ 202
                                                                                   Mismatches
                                                                                                                             AAM42355 standard; Protein; 328 AA
, 26;
                                                                                                                                                                          Human polypeptide SEQ ID NO 88
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2000US-0230437
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                                                                                                                                                          22-OCT-2001 (first entry)
   Conservative
                                                                                                                                                                                                                                                                WO200155449-A1,
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08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                   Homo sapiens
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17-NOV-2000;
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08-DEC-2000;
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   89;
                                                                                                                                            AAM42355;
   Matches
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Rosen CA, Barash SC, Ruben SM;

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WPI: 2001-476225/51.

Novel plasma membrane associated proteins useful for diagnosing, rreating, preventing and/or prognosing disorders related to the proteins, including cancer, immune response and neuronal disorders.

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Claim 11; SEQ ID NO 88; 532pp + Sequence Listing; English.

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CR AMA42347-AMA4415) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are completed from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful on the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; c) immune disorders e.g. Addison's disease, allergies, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal colitis; (c) cardiovascular disorders such as viral, bacterial, fungal printed specification, but was obtained in electronic format directly from WIPO at ftp. WiPo. int/pub/published_pct_sequences.
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515 aigtvgahrnicpnsgflrglgvldnrlgretgr 548
173 AIQQVAKNRCVLPNRGFLKQLRELDKQLVQQRRR 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: February
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to phosphatase polypeptides, nucleotide sequences encoding them, as well as various products and methods useful for the diagnosis and treatment of various phosphatase-related diseases and conditions. Substance that modulates the activity of phosphatase polypeptide is used to treat immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases and metabolic disorders, including cancers of tissues, cancers of heematopoietic origin, diseases of central and peripheral nervous system, Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, viral infections, infections caused by prions, bacteria and fungi, ocular diseases, diabetes, migraines, pain, sexual dysfunction, mood disorders, attention disorders, ognition disorders, hypotension, hypertension, psychotic disorders, neurological disorders, dyskinesias and organ transplant rejection. The present amino acid sequence is human SCPO14 phosphatase polypeptide. This sequence is classified as dual specificity phosphatase (DSP) and MAPP (Annea) and Annea) and Annea and Annea and Annea and Annea and Annea and Annea Annea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hill
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sudarsanam S,
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                                                                                                           37..181
/label- Phosphatase_domain
368..520
/label- Phosphatase_domain
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                                                                                        /label= Catalytic_domain
                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35;
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99US-0175766.
2000US-0178078.
2000US-0179301.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Martinez R,
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N-PSDB; AAD09496.
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                                                                                                                                                                                                                                 WO200146394-A2
Homo sapiens
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28-DEC-1999;
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Flanagan P;
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                                                                  Domain
                                                                                                              Domain
                                                                                                                                                            Domain
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Matches
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New human hydrolase-like molecules (HHLMS) and polynucleotides encoding
the HHLMS, useful for diagnosing, treating or preventing cell
proliferation (e.g. bone cancer) or autoimmune disorders(e.g. AIDS or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to isolated and purified cDNA encoding a human hydrolase-like molecule (HHLM), designated HHLM-1 to HHLM-8. The HHLM DNAs and polypeptides are useful for diagnosing, treating or preventing cell proliferation disorders and autoimmune disorders. Cell proliferation disorders include cancers, autoimmune disorders include AIDS (acquired immune deficiency syndrome): The present sequence is a HHLM protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39 FELERLFWKGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NC;
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                                                                                                                                                                                     Hydrolase-like molecule; human; cell proliferation disorder; autoimmune; cancer; AIDS; acquired immune deficiency syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 207;
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Pred. No. 1.2e-41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26; Mismatches
                                                                                                                                         Human hydrolase-like molcule 4 protein.
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53.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0013881.
AAB28793 standard; Protein;
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Plowman,G.D., Martinez,R., Whyte,D., Manning,G., Sudarsanam,S.,
Manmalian protein phosphatases
Patent: WO 0146394-A 5 28-JUN-2001;
Sugen, Inc. (US)
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/organism="Homo sapiens"
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                                                                    Length 159517;
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Catarrhini; Hominidae;
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Genome Therapeutics Corporation Sequencing
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Pred. No. 1.4e-100;
); Mismatches 6;
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Street, Waltham, MA 02453, USA
On May 7, 2000 this sequence versic
Location/Qualifiers
e 1.159517
/organism="Homo sapiens"
/db_xref="taxon:9606"
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32772 c 34285 g 47356
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Submitted (13-DEC-1999) Genome
Street, Waltham, MA 02453, USA
3 (bases I to 159517)
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Street, Waltham, MA 02453, USA
4 (bases 1 to 159517)
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Mammalia, Eutheria, Primates;
1 (bases 1 to 159517)
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/clone="RP11-77G23"
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/db_xref="G1:15072533" /translation="MAETSLPELGEEDKATPCPSILELEELLRACKSSCSRVDEVWPN LETGDATAPANTELLYLDAAHRGLYCOGGDDFYGSSVSYLGVPAHDLPDFD ISAYFSSAADFIHRALMTPGAKULVHCVVGVSRSATLVLAYLMLHQRLSLRQAVITVR GHRWVFPNRGFLHOLCRLDGOLRGGGS" OHRWVFPNRGFLHOLCRLDGOLRGGGS"  Misc_feature 508.1491  misc_feature 895.1491  /note="similar to testis- and muscle-expressed dual-specificity protein phosphatase, long form; TMDP-L" 895.1491  /note="similar to testis- and muscle-expressed dual-specificity protein phosphatase, short form; TMDP"  BASE COUNT 329 a 545 c 510 g 342 t	Ouery Match 17.9%; Score 208; DB 9; Length 1726; Best Local Similarity 63.4%; Pred. No. 3.5e-29; Matches 335; Conservative 0; Mismatches 190; Indels 3; Ga 192 gaggaggaggaggaggactactgcacccctggagcctttgagctggagcggctc 192 gaggaggaggaggaggaggactactgcacccttgagccttttgagctggagcggctc 11	UN   252   LCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	0y 432 gacatccagtaccacggcgtggaggccgacctgccaccttcgacctcagtgtcttc 491	RESULT 4 AX180880 LOCUS DECUSS DEFINITION Sequence 7 from Patent W00146394. ACCESSION AX180880 G1 G1:15132708 NERRINO NERRINO SOURCE ORGANISM HOMO Sapiens CRANSM HOMO Sapiens CRANSM HOMO Sapiens CRANSM HOMO Sapiens CRANSM HOMO Sapiens ATTLE AMINIA G1 G16 G16 G16 G16 G16 G16 G16 G16 G16
	901 cttgttcaacttccccatgtgtgctggggacagggaggacccagagctgccccgggcag	OY 1021 9949994049405040499190405040401010101010101010101010101010101	ACCESSION AVO40091 1726 bp mRNA PRI 01-AUG-2001 DEFINITION Homo sapiens branching-enzyme interacting dual-specificity protein phosphatase BEDP mRNA, complete cds. ACCESSION AY040091.1 GI:15072532 NEXEWORDS SOURCE Human. ORGANISM Homo sapiens EUKATYOTA; METAZOA; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. TITLE I (bases 1 to 1726) TITLE Interacts with glycogen-branching enzyme JOURNAL SKUTEACLA.V. and Dietrich, A.D. TITLE Interacts with glycogen-branching enzyme JOURNAL SKUTEACLA.V. and Dietrich, A.D. TITLE JOURNAL JOURNAL JOURNAL AUTHORS SKUTEACLA.V. and Dietrich, A.D.	JOURNAL Submitted (13-JUN-2001) Blochemistry and Molecular Biology, Indiana University School of Medicine, 635 Barnhill Dr., Indianapolis, IN 46202, USA  Location/Qualifiers  1. 1726  / Corganism="Homo sapiens" / Ab_xref="taxon:9606" / Chromosome="10" / Chromosome

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591 gtcctggcctacctgatgatccacaaggacatgacctggtggacgccatccagcaagtg 650
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1665)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (03-JAN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                      306
                                                                                                                                                                                                                                                                                                                                cccgactactaccgcgacatggacatccagtaccacggcgtggaggccgacgacctgcc 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: MGC help desk Email: cgapbs-rémail.nih.gov Tissue Procurement: DCTD/DTP CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                         9
                                                                                                              Length 636;
                                                                                                                                         Indels
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IMAGE:3535215,
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                                                                                                              9
                                                                                                                                        0; Mismatches 168;
                                                                                                           Score 204.2; DB (
Pred. No. 2.1e-28
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                          /organism="Homo sapiens"
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207 c 182 g 124
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TITLE
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VFELBRLLTGTACHTACHTADEVWPGLTLGDQDMANNRRELRRLGITHVLMASHSRWRGT
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TLVLAYLMLYHHLTLVPAIKKVKDHRGIIPNRGFLRQLLALDRRLRQGLEA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov beries: IRAL Plate: 8 Row: o Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6807668.
Location/Qualifiers
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                                                                                                                                                                        Yaron Butterfield,
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/protein_id="AAH01613.1"
/db_xref="GI:12804419"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="MGC:1136 IMAGE:3535215"
/tissue_type="Lung, small cell carcinoma"
/clone_lib="\nff,MGC_"
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Note of the control of the contro
                                                                                                                                                             Steven Jones, Jennifer Asano, Ian Bosdet,
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Pred. No. 1.8e-28;
0; Mismatches 168
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                                        BC Cancer Agency,
info@bcgsc.bc.ca
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Eukaryotan Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [1] (bases 1 to 904)
Plowman, G.D., Martinez, R., Whyte, D., Hill, R., Flanagan, P. and Lioubin, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein phosphatase.
Homo sapiens cDNA to mRNA.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
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Homo sapiens mRNA for protein phosphatase, complete cds.
ABO27004
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                             09-MAR-2001
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Pred. No. 1.6e-27;
0; Mismatches 166;
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Patent: WO 0112819-A 17 22-FEB-2001;
Sugen, Inc. (US)
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                           AX086020 904 bp DNA
Sequence 17 from Patent WO0112819.
AX086020
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/organism="Homo sapiens"
/db_xref="taxon:9606"
a 282 c 249 g 191
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                                                                  AX086020.1 GI:13275841
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Best Local Similarity 64.3%;
Matches 299; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 1917)
Plowman,G.D., Martinez,R., Whyte,D., Manning,G., Sudarsanam,S.,
Hill,R.J. and Flanagan,P.
Mammalian protein phosphatases
Patent: WO 0146394-A 6 28-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
596 c 565 g 386
                                                                                                         AXIB0879 1917 bp DNA Sequence 6 from Patent WO0146394.
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Location/Qualifiers
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Matches 328; Conserv
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/organism="Homo sapiens"
/db_xref="LocusID:51207"
/db_xref="taxon:9606"
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                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 1053)
                                                                                                                                                                                                                                                 Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host-"DH10B"
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                           BC009778
BC009778.1 GI:14602534
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298; Conservative
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                                                                                               Kikuchi, K., Nakamura, K. and Shima, H.
Kikuchi, K., Nakamura, K. and Shima, H.
Subirect Submission
Submitted (07-MAY-1999) to the DDBJ/EMBL/GenBank databases. Kunimi
Kikuchi, Hokkaido University, Section of Biochemistry, Institute of
Immunological Science: Kita-15, Nishi-7, Kita-ku, Sapporo 060-0815,
Japan (E-mail:kikuchi@imm.hokudai.ac.jp, Tel:81-11-707-6839,
                                                                                                                                                                                                                                                                                                                                                                                   HIDEVWPSLFLGDAYAARDKSKLIQLGITHVVNAAAGKFQVDTGAKFYRGMSLEYYGI
EADDNPFFDLSVYFLPVARYIRAALSVPQGRVLVHCAMGVSRSATLVLAFLMICENMT
LVEAIQTVQAHRNICPNSGFLRQLQVLDNRLGRETGRF"
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                          Nakamura,K., Shima,H., Watanabe,M., Haneji,T. and Kikuchi,K. Molecular cloning and characterization of a novel dual-specificity protein phosphatase possibly involved in spermatogenesis Biochem. J. 344 Pt 3, 819-825 (1999)
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Pred. No. 3.1e-27;
0; Mismatches 167;
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/db_xref="taxon:9606"
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/product="protein phosphatase"
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CMDA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Blology
http://www.systemsbiology.org
contact: amadamésystemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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/tissue_type="Bone marrow, chronic myelogenous leukemia"
Homo sapiens, protein phosphatase, clone MGC:13471 IMAGE:4047963, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (02-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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298 c 298 g 209 t
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Pred. No. 3e-27;
0; Mismatches 167;
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셤 õ g ò g ò g ò g

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/translation-"MSIHFOTAADFIHRALSOPGGKILVHCAVGVSRSATLVLAYLML
YHHLTLVEAIKKVKDHRGIIPNRGFLRQLLALDRRLRQGLEA"
346 c 379 q 220 t
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Bandman,O., Lal,P., Hillman,J.L., Corley,N.C., Guegler,K.J. and
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                                                                                                                                                               16.6%; Score 193.8; DB 9 64.8%; Pred. No. 1.6e-26; iive 0; Mismatches 167
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Patent: US 6132964-A 12 17-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submittae (13-FEB-2001) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                             BC003115 1243 bp mRNA PRI 12-JUL-2001
Homo sapiens, clone MGC:2627 IMAGE:3502718, mRNA, complete cds.
BC003115
                                                                                                                            cggtcagccacctggtcctggcctacctgatgatccacaaggacatgacctggtggac 635
                                                                                                                                             gacagagcgctaagcgacgaccacagtaagatcctggttcactgcgtcatgggccgcagc
                                                                                       559 CGAGCTGCCCTCAGTGTTCCCCAAGGCCGCGTGCTGGTACACTGTGCCATGGGGGTAAGC
                                                                                                                                                                                                   gccatccagcaagtggccaagaaccgctgcgtcctcccgaaccggggctttttgaagcag
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                      696 ctccgggagctggacaagcagctggtgcagcagaggcgacggtcc 740
                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:2627 IMAGE:3502718"
/tissue_type="Brain, neuroblastoma"
/clone_lib="NIH_MGC_19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
Context: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         George Yang, Scott Zuyderduyn, Marco Marra.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg, R.
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Kikuchi, K., Nakamura, K. and Shima, H.

Direct Submission

Direct Submission

Submitted (07-MX-1999) to the DDBJ/EMBL/GenBank databases. Kunimi
Kikuchi, Hokkaido University, Section of Biochemistry, Institute of
Immunological Science; Kita·15, Nishi-7, Kita-ku, Sapporo 060-0815,
Japan (E-mail: kikuchi@imm.hokudai.ac.jp, Tel:81-11-707-6839)
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HINWWPWINELGDAYARDKGRLIQLGITHVVNVAAGKFQVDTGAKFYRGTPLEYYGI
EADDNPFEDLSVHFLPVARYIRDALNIPRSRYLVHCAMGVSRSATIVLAFLMIFENWT
LVDAIQTVQAHRDICPNSGFLRQLOVLDNRIERRETGRL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (sites)
Nakamura,K., Shima,H., Watanabe,M., Haneji,T. and Kikuchi,K.
Molecular cloning and characterization of a novel dual-specificity
protein phosphatase possibly involved in spermatogenesis
Biochem. J. 344 Pt 3, 819-825 (1999)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                   411 cccgactactaccgcgacatggacatccagtaccacggcgtggaggccgacgacctgcc 470
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                   291 gictggcccaagcictacattggcgatgaggcgacggcgctggaccgctataggctgcag 350
                                                                                                                                                                                                                                          AB027003 686 bp mRNA ROD 13-JAN-2000 Mus musculus mRNA for protein phosphatase, complete cds.
                                                                                                               CAGCTGGGCATTACCCATGTTGTGAATGTGGCTGCGGCCAAGTTCCAGGTGGACACGT
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/protein_id="BAA89411.1"
/db_xref="G1:6692780"
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Mus musculus CDNA to mRNA.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

1 (bases 1 to 597)

Plowman, G.D., Martinez, R., Whyte, D., Hill, R., Flanagan, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291 gtctggcccaagctctacattggcgatgaggcgacggcgctggaccgctataggctgcag 350
                                                                                                                                                                                    351 aaggoggggttcacgcacgtgctgaacgcggcccacggccgctggaacgtggacactggg 410
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); Mismatches 165; Indels
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Pred. No. 4e-21;
); Mismatches 213;
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Patent: WO 0112819-A 7 22-FEB-2001;
Sugen, Inc. (US)
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/organism="Mus sp."
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/organism="Homo sapiens"
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Aoyama, K., Matsuda, T. and Aoki, N.
Molecular cloning of a novel dual specificity phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1094 bp mRNA ROD 02-MAR-2001 dual-specificity phosphatase TS-DSP6 mRNA, complete
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Aoyama, K., Matsuda, T. and Aoki, N.
Direct Submission
Submitted (19-FEB-2000) Applied Molecular Biosciences, Nagoya
University, Furo-cho, Chikusa-ku, Nagoya, Aichi 464-8601, Japan
Location/Qualifiers
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                                                                                  231 gcctttgagctggagcggctcttctggaagggcagtccccagtacacccacgtcaacgag 290
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EADDAWFFDLSVHFLPVARYIRDALMIPRSRVLVHCAMGVSRSATIVLAFLMIPENMT
LVDALQTVQAHRDICPNSGERQLQVLDNRLRREFGRL"
293 C 327 t 3 others
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom;
Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.
1 (bases: 10.4360)
Plowman.G.D., Martinez,R., Whyte,D., Manning,G., Sudarsanam,S.,
Hill,R.J. and Flanagan,P.
Mammalian protein phosphatases
Patent: WO 0146394-A 4 28-JUN-2001;
Sugen, Inc. (US)
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Pred. No. 3.5e-21;
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Pred. No. 1.1e-17;
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 Query Match 12.5%;
Best Local Similarity 58.2%;
Matches, 296; Conservative
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Search completed: February 8, 2002, 18:42:47 Job time: 4317 sec

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Sequence 8, N. Sequence 5, A. Sequence 2, A. Sequence 2, A. Sequence 20, A. Sequence 20, A. Sequence 23, Sequence 2, A. Sequence 1, A. Sequence 13, Sequence 11, A. Sequence 1

Sequence

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APPLICANT: Acton, Susan
TITLE OF INVENTION: No. 6268135el Phospholipase Molecule and Uses Therefor
FILE REFERENCE: min.059
CURRENT APPLICATION NUMBER: US/09/163,833
CURRENT FILING.DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 198
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                    US-08-446-363-3
US-08-015-985-8
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US-08-164-193-2
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US-09-041-886-13
US-08-015-973-1
US-08-448-164-1
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                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09163833 Patent No. 6268135 GENERAL INFORMATION:
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Patent No. 6132964
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Sequence 21, Appl
Sequence 2, Appli
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                                                                                    Search time 12.62 Seconds
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-164-193-5
US-08-184-273-2.
US-08-164-193-21
US-09-164-193-21
US-09-164-193-21
US-07-988-273-3
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Maximum Match 100%
Listing first 45 summaries
                                                          protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Post-processing:

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Title: Perfect score:

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Indels

Bandman, Olga Lal, Preeti Hillman, Jennifer L. Corley, Neil C. Guegler, Karl J.

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Sequence

166 157.5 142.5 142.5 128.5 123 113 102.5 100.5

5-08-933-750C-21 5-09-234-613-21 5-07-988-273-5

Sequence Sequence Sequence Sequence Sequence Sequence

346.5 346.5 346.5 346.5 346.5 2247.5 192.5 192.5 1188.5 177.5 169

Result Š.

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41 LERLFWKGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDY 100
                                                                                                                                                                                                                                                     101 YRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 GAFE----LERLFWKGSPQYT----HVNEVWPKLYIGDEATALDRYRLQKAGFTHVLNA
                                                                                                                                     2;
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                                                                                                Length 263;
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                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: AARONSON, Stuart A.
APPLICANT: BOTTARO, Donald P.
APPLICANT: ISHIBASHI, Toshio
APPLICANT: MIKI, Toru
TITLE OF INVENTION: EXPRESSION CLONING OF A HUMAN
TITLE OF INVENTION: PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/988,273 FILING DATE: 19921214
                                                                                            31.3%; Score 363; DB 4; L 51.8%; Pred. No. 3.6e-34; Live 22; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
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Pred. No. 1.8e-32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 19921214
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 4039
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/07988273
Patent No. 5512434
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEE: Foley & Lardner: 3000 K Street, N.W., Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                      123 YLMLYHHLTLVEAIKKVKDHR 143
                                                                                                                                                                                                                                                                                                                                  161 YLMIHKDMTLVDAIQOVAKNR 181
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43.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: .(202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 amino acids
AMINO ACID
                                                                                              Query Match 31.3'
Best Local Similarity 51.8'
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 29.8%
Best Local Similarity 43.8%
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                  ORGANISM: Homo sapiens
JS-09-164-193-5
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US-07-988-273-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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Patent No. 6258582
GENERAL INFORMATION:
ATICIANT: Acton, Susan L.
TITLE OF INVENTION: NOVEL CSAPTP NUCLEIC ACID MOLECULES AND USES THEREFOR (as amended FILE REFERENCE: MNI-051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46 FELERLLYTGKTACNHADEVWPGLYLGDQDMANNRRELRRLGITHVLNASHSRWR--GTP 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 DYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; DB 4; Length 207; 1.2e-41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      159 LAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQLVQ 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 LAYLMLYHHLTLVBAIKKVKDHRGIIPNRGFLRQLLALDRRLRQ 203
              TITLE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES WIMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS: . ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                         MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSRO for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26; Mismatches
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CURRENT FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 23
SOFWARE: Patentin Ver. 2.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36.7%; Score 426; 53.0%; Pred. No. 1
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                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/013,881
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-845-0555
TELEFAX: 650-845-4166
                                                                                        Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 207 amino acids
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Shah, Purvi
                                                                                                                                                                   ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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CLONE: 971204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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Best Local Similarity
Matches 87; Conserv
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                                                                                                                                                       USA
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US-09-164-193-5
                                                                                                                                                     COUNTRY:
                                                                                          STREET:
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Length 185;

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GENERAL INFORMATION:
APPLICANT: ACLOM, Susan L.
TITLE OF INVENTION: NOVEL CSAPTP NUCLEIC ACID MOLECULES AND USES THEREFOR (as amerILE REFERENCE: MNI-051
CURRENT APPLICATION NUMBER: US/09/164,193C
CURRENT FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PATEHILN Ver. 2.0
SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 AHGR--WNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILV 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                  37 GAFE----LERLFWKGSPQYT----HVNEVWPKLYIGDEATALDRYRLQKAGFTHVLNA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 GAFE----LERLFWKGSPQYT----HVNEVWPKLYIGDEATALDRYRLQKAGFTHVLNA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      146 HCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQLVQQ 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXPRESSION CLONING OF A HUMAN PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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Pred. No. 1.8e-32;
5; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                29.8%; Score 346.5; DB 4
43.8%; Pred. No. 1.8e-32;
Live 35; Mismatches 54
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                      Application US/09164193C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 14-DEC-1992
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 29.8%
Best Local Similarity 43.8%
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 43.89
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein
PCT-US93-12019-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: PHOUMBER OF SEQUENCES: 7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
US-09-164-193-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC
OPERATING SYSTEM:
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                      Sequence 21, Applior
Patent No. 6258582
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JS-09-164-193-21
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                    88 AHGR--WNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILV 145
                                            88 AHGR--WNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILV 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 HCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQLVQQ 203
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                                                                                                                    11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3; Length 185;
                                                                                                                                                                                                                                                                                                                                      Catalytic Macro Molecules Having DCD25B
Like Activity
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; Pred. No. 1.8e-32;
35; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                          3: Pharmacia & Upjohn Company
301 Henrietta Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                              Sequence 25, Application US/08848810 Patent No. 6074851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: WOOLLON, Thomas A.
REGISTRATION NUMBER: 35,004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616-833-7914
TELEFAX: 616-833-6897
                                                                                                                                                                                                                                                                                  APPLICANT: Deidel Jr., M. R.
APPLICANT: Yem, A. W.
APPLICANT: Wilson, C. L.
TITLE OF INVENTION: Catalytic
TITLE OF INVENTION: Like Activ
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 25: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 185 amino acids
amino acid
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Matches 78; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: 1in
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49001
                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                            US-08-848-810-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-848-810-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
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AHGR--WNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILV 145 

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RESULT

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Indels 11; Gaps

Length 185;

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Length 118;

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GENERAL INFORMATION:
APPLICANT: Stork, Philip J
APPLICANT: Stork, Philip J
APPLICANT: Stork, Philip J
APPLICANT: Misra-Press, Anita
TITLE OF INVENTION: Mitogen Activated Protein Kinase Phosphatase cDNAs and
TITLE OF INVENTION: Their Biologically Active Expression Products
TITLE OF INVENTION: Their Biologically Active Expression Products
FILE REFERENCE: 4104 000332USA
CURRENT APPLICATION NUMBER: US/08/990,379
CURRENT FILING DATE: 1997-12-15
EARLIER APPLICATION NUMBER: FCT/US96/10402
BARLIER FILING DATE: 1996-06-16
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 VLNAAHGR--WNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAA-AFIDRALSDDH 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 EVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197 EILPFLYLGSAYHAARRDMLDALGITALLNVS-----SDCPNHF-EGHYQYKCIPVEDN 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 PIFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQ 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 SKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELD 197
                                                PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                     21.3%; Score 247.5; DB 5; ilarity 47.0%; Pred. No. 3e-21; Conservative 24; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 16.6%; Score 192.5; DB 2; Best Local Similarity 34.2%; Pred. No. 4.4e-14; Matches 50; Conservative 29; Mismatches 58;
                                                                                                  PCT/US93/12019
                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,273
FILING DATE: 14-DEC-1992
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177 VAKNRCVL-PNRGFLKQLRELDKQLV 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08990379 Patent No. 5998188
                                                                                                                                                                                                                                                                          : 118 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Rattus norvegicus
                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 55; Conserv
                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                              PCT-US93-12019-3
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63 AEGRSFMHVNTNANFYKDSGITYLGIKANDTQEFNLSAYFERAADFIDQALAQKNGRVLV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VLNAAEGRSFWHVNTNANFYKDSGITYLGIKANDTQEFNLSAYFERAADIFIDQALAQKN 60
                                                                              123 HCREGYSRSPTLVIAYLMMRQKMDVKSALSIUVRQNREIGPNDGFLAQLCQLNDRLAKE 180
                                             146 HCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQLVQQ 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 SKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELD 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.3%; Score 247.5; DB 1; Length 118; 47.0%; Pred. No. 3e-21; ive. 24; Mismatches 35; Indels 3
                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: AARONSON, Stuart A.
APPLICANT: BOTTANO, Donald P.
APPLICANT: ISHIBASHI, TOSHIO
APPLICANT: MIKI, TOTU
TITLE OF INVENTION: EXPRESSION CLONING OF A HUMAN
TITLE OF INVENTION: PHOSPHATASE
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OFERALIZE SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/988,273 FILING DATE: 19921214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                  Sequence 3, Application US/07988273
Patent No. 5512434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 40
FELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 904136
INFORMATION FOR SEQ ID NO: 3:
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ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
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AMINO ACID
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Best Local Similarity 47.0%
Matches 55; Conservative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
STREET: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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PCT-US93-12019-3
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309

EXPRESSION CLONING OF A HUMAN PHOSPHATASE

NUMBER OF SEQUENCES: 7 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

TITLE OF INVENTION: TITLE OF INVENTION:

RESULT 11

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Sequence 7, Application US/08990379
Patent No. 598188
GENERAL INFORMATION:
APPLICANT: Stork, Philip J
APPLICANT: Stork, Philip J
APPLICANT: Stork, Philip J
APPLICANT: Misra-Press, Anita
TITLE OF INVENTION: Micogen Activated Protein Kinase Phosphatase cDNAs and
TITLE OF INVENTION: Micogen Activated Protein Kinase Phosphatase CDNAs and
TITLE OF INVENTION: Micogen Activated Protein Kinase Phosphatase CDNAs and
TITLE OF INVENTION: Micogen Activated Protein Kinase Phosphatase CDNAs and
TITLE OF INVENTION: Micogen Activated Protein Kinase Phosphatase CDNAs and
TITLE OF INVENTION: UMBER: US/08/990,379
CURRENT APPLICATION NUMBER: US/08/10402
EARLIER APPLICATION NUMBER: 60/000,263
EARLIER PILING DATE: 1996-06-14
EARLIER FILING DATE: 1995-06-16
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 PTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQ 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MTSGEVKTSLKNAYSSAKRLSPKMEEEGEEEDYCTPGAFELER-----LFWKGSPQYTHV 55
APPLICANT: Stork, Philip J
APPLICANT: Stork, Philip J
APPLICANT: Misra-Press, Anita
TITLE OF INVENTION: Mitogen Activated Protein Kinase Phosphatase CDNAS
TITLE OF INVENTION: Their Biologically Active Expression Products
TITLE OF INVENTION: Their Biologically Active Expression Products
FILE REPRENCE: 4104-0003220SA
CURRENT APPLICATION NUMBER: US/08/990,379
CURRENT FILING DATE: 1997-12-15
EARLIER APPLICATION NUMBER: PCT/US96/10402
EARLIER PILING DATE: 1995-06-16
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.6%; Score 192.5; DB 2; 34.2%; Pred. No. 4.4e-14; tive 29; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
16.2%; Score 188.5; DB 2;
Best Local Similarity 28.0%; Pred. No. 9.2e-14;
Matches 58; Conservative 39; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 VAKNRCVL-PNRGFLKQLRELDKQLV 201
                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT; ORGANISM: Rattus norvegicus
US-08-990-379-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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US-08-990-379-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 PTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQ 176
                                                                    APPLICANT: Marshall, Christopher John
APPLICANT: Ashworth, Alan
APPLICANT: Hughes, David Anthony
TITLE OF INVENTION: Methods for Screening of Substances for
TITLE OF INVENTION: Therapeutic Activity and Yeast for Use Therein
CORRESPONDENCE: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                 E: Townsend and Townsend and Crew LLP Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 192.5; DB 2,
; Pred. No. 4.4e-14;
29; Mismatches 58
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APPLICATION NUMBER: WO PCT/GB94/00694
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9402573.1
FILING DATE: 10-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9307250.2
FILING DATE: 07-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 14-DEC-1995
CLASSIFICATION: 435
IOR ADDITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 VAKNRCVL-PNRGFLKQLRELDKQLV 201
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 23, Application US/08530290 Patent No. 5958721 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 0846:
TELECOMMUNICATION INFORMATION:
TELEFANE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/08990379; Patent No. 5998188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 34.2%;
Matches 50; Conservative 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: peptide US-08-530-290-23
                                                                                                                                                                                                                                                                                                  CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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US-08-990-379-5
                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
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80 GFTHVLNAA----HGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRA 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 LSPKMEEEGEEEDYCTPGAFELERLFWKGSPQYTHVNEVWPKLYIGDEATALDRYRLQKA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 MAPRMISEGD-------IGGIAQITSSLFLGRGSVASNRHLLQAR 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 GITCIVNATIEIPNFNW-----PQF-----EYVKVPLADMPHAPIGLYFDTVADKI-HS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.3%; Score 177.5; DB 4; 28.5%; Pred. No. 8.9e-13; iive 33; Mismatches 61;
OPERATING SYSTEM: DOS SOFTWARE: FASICED for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,973
FILING DATE: Filed Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: February 8, 2002, 15:42:02
                                                                                                                                                                                                                                                 PF-0491 US
                                                                                                                                                                                                         NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 198 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 28.53
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS:/ single
                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    INMEDIATE SOURCE:
LIBRARY: BRSTNOT16
CLONE: 3041794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    195 ELDKQL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : ::||
160 DYERQL 165
                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Job time: 121 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-045-973-5
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                                                                                                                                                                                                                                                                                                                          APPLICANT: Acton, Susan L.
TITLE OF INVENTION: NOVEL CSAPTP NUCLEIC ACID MOLECULES AND USES THEREFOR (as amended FILE REPERENCE: MN-7051
CURRENT APPLICATION NUMBER: US/09/164,193C
CURRENT FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
  ---ASCPNHFEGL-FHYKSIPVED 225
                                        116 LPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQ 175
                                                              226 NQMVEISAWFQEAISFID-SVKNSGGRVLVHCQAGISRSATICLAYLIQSHRVRLDEAFD 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 LRGGFKSFQTYCPDLCSEAPAQALPPAGAENSNSDPRVPIYDQGGPV----EILPYLYI 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 GDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVF 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 GSCNHSSDLQGLQACGITAVLNVS-----ASCPNHFEGL-FHYKSIPVEDNQMVEISAW 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 FYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 LKNAYSSAKRLSPKMEEEGEEEDYCTPGAFELER----LFWKGSPQYTHVNEVWPKLYI 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Yue, Helly
APPLICANT: COTIEY, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah
TITLE OF INVENTION: PROTEIN PHOSPHATASE RELATED MOLECULES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.9%; Score 184.5; DB 4; Length 314; 28.3%; Pred. No. 2.7e-13; Live 39; Mismatches 84; Indels 19;
174 -EILPYLYLGSCNHSSDLQGLQACGITAVLNVS---
                                                                                                                     176 QVAKNRCVL-PNRGFLKQLRELDKQLV 201
| : | |: | |: || :| ::
285 FVKQRRGVISPNFSFMGQLLQLETQVL 311
                                                                                                                                                                                                                                             US-09-164-193-22
Sequence 22, Application US/09164193C
Patent No. 6258582
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-045-973-5; Sequence 5, Application US/09045973; Patent No. 6165767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 -PNRGFLKQLRELDKQLV 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Yue, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Mus musculus US-09-164-193-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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protein - protein search, using sw model

8, 2002, 15:43:46; Search time 23.54 Seconds February Run on:

(without alignments) 692.274 Million cell updates/sec

US-09-847-519A-2

220 1 MTSGEVKTSLKNAYSSAKRL.....VQQRRRSQRQDGEEEDGREL 220 score: Sequence: Perfect

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

522463 segs, 74073290 residues Searched:

10 Word size : Total number of hits satisfying chosen parameters:

1

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

/SiDSB/gcgdata/geneseqp/Aa1980.DAT:\*
/SiDSB/gcgdata/geneseqp/AA1981.DAT:\*
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/SiDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:\*
/SiDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:\*
/SiDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:\*
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/SiDSB/gcgdata/geneseq/geneseqp/AA1991.DAT:\*
/SIDSB/gcgdata/geneseq/geneseqp/AA1991.DAT:\* A\_Geneseq\_1101:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:\* /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:\*

SUMMARIES

	Description	Human SGP003 phosp	A human requiator	Human SGP014 phosp	Human polypeptide	Human hydrolase-li	Human dual specifi	Human polypeptide	Human SGP060 phosp	Human cardiovascul	Human polypeptide	Human SGP014 phosp
	ID	AAE04837	AAB18667	AAE04849	AAM41142	AAB28793	AAY85620	AAM39356	AAE04839	AAY92175	AAM42355	AAE04838
	DB	22	21	22	22	22	21	22	22	21	22	22
	Query e Match Length DI	220	221	57	80	207	211	211	211	263	328	549
æ	Query Match	61.4	44.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5
	Score	135	86	12	12	12	12	12	12	12	12	12
	Result No.		7	co	4	ស	o	7	œ	6	10	11

## ALIGNMENTS

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Human; SGP003 phosphatase polypeptide; phosphatase-related disease; infimune-related disorder; ocular disease; organ transplant rejection; infection; diabetes; pain; sexual dysfunction; Alzhedmar's disease; metabolic disorder; haematopoletic cancer; mood disorder; cardiant; Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; cardiovascular disease; brain; neuronal-associated disease; dyskinesia; attention disorder; cognition disorder; psychotic disorder; cytostatic; neurological disorder; virucide; nootropic; cerebroprotective; therapy; neurological disorder; virucide; nootropic; cerebroprotective; therapy; hypotensive; immunosuppressive; antipsoriatic; antiasthmatic; hypotensive; immunosuppressive; antipsoriatic; analgesic; hyportensive; antigraine; chromosome CHR10.
                                                                                     Human SGP003 phosphatase polypeptide.
                     AAE04837 standard; Protein; 220 AA
                                                                (first entry)
                                                                10-SEP-2001
          AAE04837
RESULT
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Homo sapiens

54..199 /label- Phosphatase\_domain /label- Catalytic\_domain Location/Qualifiers 82 Misc-difference Domain Domain

/note- "Encoded by CTG"

WO200146394-A2

28-JUN-2001

21-DEC-2000; 2000WO-US34736

21-DEC-1999; 99US-0173255. 28-DEC-1999; 99US-0175766. 25-JAN-2000; 2000US-0178078. 31-JAN-2000; 2000US-0179301 21-DEC-1999; 28-DEC-1999;

(SUGE-) SUGEN INC.

ξ; Martinez R, Whyte D, Manning G, Sudarsanam S, Hill Plowman GD, Flanagan P;

WPI; 2001-418058/44. N-PSDB; AAD09495.

Novel phosphatase polypeptide useful for treating cancers, immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases and metabolic disorders

Claim 7; Fig 2; 186pp; English.

The present invention relates to phosphatase polypeptides, nucleotide sequences encoding them, as well as various products and methods useful for the diagnosis and treatment of various phosphataser-related diseases and conditions. Substance that modulates the activity of phosphatase polypeptide is used to treat immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases and metabolic disorders, including cancers of tissues, cancers of haematopoietic origin, diseases of central and peripheral nervous system, Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, viral infections, infections caused by

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17-MAR-2000; 2000WO-US07277
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                                                       20-MAY-1999;
09-JUL-1999;
                                       18-MAR-1999;
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ID AAE04
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prions, bacteria and fungi, ocular diseases, diabetes, migraines, pain, sexual dysfunction, mood disorders, attention disorders, cognition disorders, hypotension, hypertension, psychotic disorders, neurological disorders, dysfinesias and organ transplant rajection. The present amino acid sequence is human SCPO03 phosphatase polypeptide. This sequence is classified as dual specificity phosphatase (DSP) and MAP Kinase phosphatase (MKP). SGPO03 gene maps to chromosomal position
                                                                                                                                                                                                                                                                      86 NAAHGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILV 145
                                                                                                                                                                                                                                                                                          146 HCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQLVQQRR 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "tyrosine specific protein phosphatase active
    site"
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; Intracellular phosphorylation regulator; HRIP; stroke; myelon neurological disorder; Parkinson's disease; demyelinating disease; meningitis; developmental disorder; neuromuscular disorder; cancer; maysthenia gravis; cell proliferative disorder; actinic keratosis; arteriosclerosis; atherosclerosis; leukaemia; melanoma; bronchitis; autorimune disorder; inflammantory disorder; Addison's disease; acquired immunodeficiency disease; allergy; diabetes mellitus; rheumatoid arthritis; microbial infection; trauma.
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                                                                                                                                                                                                      Length 220;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A human regulator of intracellular phosphorylation.
                                                                                                                                                                                                     61.4%; Score 135; DB 22; I
100.0%; Pred. No. 5.3e-128;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphorylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                      Matches 135; Conservative
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                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                      220 AA;
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                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB18667
                                                                                                                                                                                                        Query Match
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AAB18667
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neuromuscular disorders, mysthenia gravis, cell proliferative disorders such as actinic keratosis, arteriosclerosis, atherosclerosis and cancer including leukaemia, melanoma, myeloma and cancer of the adrenal gland, bladder, bone, bone marrow, liver, lung, muscle, ovary, autolmmune/ inflammatory disorder such as Addison's disease, acquired immunodeficiency diseases, allergies, bronchitis, diabetes mellitus, rheumatoid arthritis, microbial infection and trauma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; cardiovascular disease; brain; neuronal-associated disease; dyskinesia; attention disorder; cognition disorder; psychotic disorder; cytostatic; neurological disorder; virucide; nootropic; cerebroprotective; therapy; neuroprotective; antibacterial; vulnerary; tranquilliser; antiasthmatic; hypotensive; immunosuppressive; antipsoriatic; analgesic; hypertensive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a human regulator of intracellular phosphorylation (HRIP). HRIP is useful for screening agonists and antagonists of HRIP polypeptide. HRIP and its agonist or antagonist are useful for treating a disease or condition associated with decreased or increased expression of functional HRIP. Diseases treated or dispanced include meurological disorders such as stroke, Parkinson's disease, demyelinating diseases, bacterial and viral menigitis and other developmental disorders of the central nervous system,
                                                                                                                                                                                                                                                                                                                                                              Novel human intracellular phosphorylation regulator polypeptides and polynucleotides for diagnosis, prevention and treatment of neurological, cell proliferative and autoimmune/inflammatory disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MTSGEVKTSLKNAYSSAKRLSPKMEEEGEEEDYCTPGAFELERLFWKGSPQYTHVNEVWP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; SGP014 phosphatase polypeptide; phosphatase related disease; immune related disorder; ocular disease; organ transplant rejection; infection; disbates; pain; sexual infection; Alzheimer's disease; metabolic disorder; hamatopoietic cancer; mood disorder; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                           Baughn MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphatase polypeptide related exon 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 98; DB 21; I
Pred. No. 1.1e-90;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 KLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGP
                                                                                                                                                                                     Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 84-85; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.5%; Scc.
100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE04849 standard; Protein; 57
                                                                                                                                                                                     Yue H,
99US-0125593.
99US-0135049.
99US-0143188.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 98; Conservative
                                                                                                                          (INCY-) INCYTE FHARM INC
                                                                                                                                                                                  Tang YT,
                                                                                                                                                                                                                 Au-Young J;
                                                                                                                                                                                                                                                                       WPI; 2000-602121/57.
N-PSDB; AAA75684.
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral neropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, anyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note: The sequence data for this patent did not form part of the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      assays for receptor activity, arthritis and inflammation, leukaemias and
    amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries \dot{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Asundi V, Chen R, Ma Y,
Wehrman T, Xu C, Xue AJ,
Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; SEQ ID NO 6073; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 5.5%; Score 12; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 12; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human hydrolase-like molcule 4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB28793 standard; Protein; 207
                                                                                                                                                                                                                                                                                                                                     2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
                                                                                                                                                                                                                          26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                                 2000US-0598042
                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0727344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 SRSATLVLAYLM 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-442253/47.
N-PSDB; AAI60298.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu C, }
Wang Z, $
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.N.S disorders
                                                                                                                                     WO200153312-A1.
                                                                                                                                                                                                                                                                                                              09-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                          29-NOV-2000;
                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                            03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                 14-SEP-2000;
                                                                                                                                                                                                                                                                     21-JAN-2000;
25-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-FEB-2001
                                                                                                                                                                                26-JUL-2001
                                                  leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang YT,
Wang J, V
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorders, hypotension, hypertension, psychotic disorders, neurological disorders, dyskinesias and organ transplant rejection. The present amino acid sequence is human SCP014 phosphatase polypeptide related exon.
SCP014 sequence is classified as dual specificity phosphatase (DSP) and MAP kinase phosphatase (MKP). SCP014 gene maps to chromosomal position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequences encoding them, as well as various products and methods useful for the diagnosis and treatment of various phosphatase-related diseases and conditions. Substance that modulates the activity of phosphatase polypeptide is used to treat immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases and metabolic disorders, including cancers of tissues, cancers of haemacopoletic origin, diseases of central and peripheral nervous system. Alzheimer's disease, Parkinson's disease, multiple sclerosis, ammyotrophic lateral sclerosis, viral infections, infections caused by prions, bacteria and fund, coular diseases, diabetes, migraines, pain, sexual dysfunction, mood disorders, attention disorders; cognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel phosphatase polypeptide useful for treating cancers, immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases and metabolic disorders
                                                                                                                                                                                                                                                                                                                                                                                                   Hill RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; ceuropathy; central nervous system; CNS; Alzheimer's; Parkinson's.disease; Huntington's disease; haemostatic;
antifungal; dual specificity phosphatase; DSP; MAP kinase phosphatase; MKP; migraine; chromosome 10q21.3; exon 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention relates to phosphatase polypeptides, nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 12; DB 22; I
Pred. No. 0.00016;
                                                                                                                                                                                                                                                                                                                                                                                                   Manning G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 127; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   Whyte D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM41142 standard; Protein; 80 AA.
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100.0%; Pre
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                                                                                                                                                                                                                                            21-DEC-1999; 99US-0173255.
28-DEC-1999; 99US-0175766.
25-JAN-2000; 2000US-0178078.
31-JAN-2000; 2000US-0179301.
                                                                                                                                                                                                21-DEC-2000; 2000WO-US34736.
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                                                                                                                                                                                                                                                                                                                                                                                                   Martinez R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152 SRSATLVLAYLM 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SUGE-) SUGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 AA;
                                                                                                           WO200146394-A2
                                                                  Homo sapiens.
                                                                                                                                                                                                                                          21-DEC-1999;
28-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                 Plowman GD,
Flanagan P;
                                                                                                                                                       28-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM41142;
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Wang D;

Ren F, W Zhang J;

Qian XB, Yang Y,

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Gaps

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Length 80; Indels

DB 22; L 0.00022;

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WPI; 2000-656232/63.
N-PSDB; AAC61100.
           Wei B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JUL-2001
          Luche RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 leukaemia
                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM39356;
                                                                                     survival
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
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                                                                                                                                                                                                    New human hydrolase-like molecules (HHLMs) and polynucleotides encoding the HHLMs, useful for diagnosing, treating or preventing cell proliferation (e.g. bone cancer) or autoimmune disorders(e.g. AIDS or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dual specificity phosphatase-9; DSP-9; human; cytostatic; cell growth; immunosuppressive; antiallergic; antiproliferative; autoimmune disease; cancer; graft-versus-host disease; allergy; metabolic disorder.
                                                                                                                                                                                                                                                                    The present invention relates to isolated and purified cDNA encoding a human hydrolase-like molecule (HHIM), designated HHIM-1 to HHIM-8. The HHLM DNAs and polypeptides are useful for diagnosing, treating or preventing cell proliferation disorders and autoimmune disorders. Cell proliferation disorders and autoimmune disorders. Cell ALDS (acquired immune deficiency syndrome). The present sequence is a HHLM protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                       Lal P, Corley NC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human dual specificity phosphatase-9 (DSP-9) amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                              ;
0
         Hydrolase-like molecule; human; cell proliferation disorder;
autoimmune; cancer; AIDS; acquired immune deficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                           5.5%; Score 12; DB 22; Length 207; 100.0%; Pred. No. 0.00052; ive 0; Mismatches 0; Indels
                                                                                                                                                      Bandman O, Hillman JL, Guegler KJ, Shah P,
                                                                                                                                                                                                                                                 Claim 1; Column 47-48; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY85620 standard; Protein; 211 AA.
                                                                                             98US-0013881
                                                                                                                98US-0013881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0128203
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Les 12; Conservative
                                                                                                                                   (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                 152 SRSATLVLAYLM 163
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-006133/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CEPT-) CEPTYR INC
                                                                                                                                                                                                                                                                                                                                                207 AA;
                                                                                                                                                                                   N-PSDB; AAC60226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200060100-A1.
                                      Homo sapiens
                                                                                             06-FEB-1998;
                                                                                                                06-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                        US6132964-A
                                                                           17-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY85620;
                                                                                                                                                                                                                                 asthma)
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Matches
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This invention relates to an isolated dual specificity phosphatase-9 (DSP-9) and its variant. The DSP-9 protein has the ability to dephosphorylate an activated mitogen activated protein (MAP) kinase.

C dephosphorylate an activated mitogen activated protein (MAP) kinase.

C included in the invention are an expression vector comprising a polynucleotide encoding the DSP-9 protein, a host cell transformed by the expression vector, and an antibody that specifically binds to DSP-9.

C DSP-9 has cytostatic; immunosuppressive; antiallargic; and antiprolliferative response, differentiallargic; and modulating a prolliferative response, differentiallard of a cell which displays contacting inhibition of cell growth, anchorage independent growth or an altered intercellular adhesion property, in a patient. DSP-9 activity such as Duchenne muscular disorder associated with DSP-9 activity such as Duchenne muscular disorder associated with DSP-9 activity such as Duchenne muscular cystrophy, cancer, graft-versus-host disease, autoimmune disease, allergies, metabolic disease, abnormalities. The present sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                  the
Dual specificity phosphatase-9 which dephosphorylates activated mitogen-activated protein kinase, used to identify agents that inhibit DSP-9 activity and modulate cell proliferation, differentiation, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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0
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100.0%; Pred. No. 0.00053;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                           Claim 1; Fig 2A; 66pp; English.
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2000US-0552317.
2000US-0598042.
2000US-0620312.
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Best Local Similarity 100.us
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Domain
                            Domain
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                                                                                                                                                                                                                           The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as paripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; SGP060 phosphatase polypeptide; phosphatase-related disease; immune-related disorder; ocular disease; organ transplant rejection; infection; diabetes; path; sexual dysfunction; Alzhelmer's disease; metabolic disorder; haematopoietic cancer; mood disorder; cardiant; Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; cardiovascular disease; brain; neuronal-associated disease; dyskinesia; attention disorder; cognition disorder; psychotic disorder; cytostatic; neurological disorder; virucide; nootropic; cerebroprotective; therapy; neurological disorder; antibacterial; vulnerary; tranquilliser; antiasthmatic; hypotensive; immunosuppressive; antipsoriatic; antischmatic; antigralie; chromosome 8pll.1-q11.1.
                                                                                                                                                                                                                                                                                                                                                                                                          The sequence data for this patent did not form part of the printed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries \mbox{-}
                                                                          Ren F, War Zhang J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.5%; Score 12; DB 22; Length 211; Best Local Similarity 100.0%; Pred. No. 0.00053; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                          Qian XB,
Yang Y,
                                                                         Asundi V, Chen R, Ma Y, (
Wehrman T, Xu C, Xue AJ,
Goodrich R, Drmanac RT;
                                                                                                                                                                                                    Example 4; SEQ ID NO 2501; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human SGP060 phosphatase polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                          Liu C, Asundi V, Wang Z, Wehrman T,
14-SEP-2000; 2000US-0662191.
19-OCT-2000; 2000US-0693036.
29-NOV-2000; 2000US-0727344.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-442253/47
                                                                                                   Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                               211 AA;
                                                 (HYSE-) HYSEQ INC
                                                                                                                                        N-PSDB; AAI58512
                                                                                                                                                                                                                                                                                                                                                                                    assays for recept C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                      specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo saptens
                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence
                                                                                       Wang J, W
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE04839;
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                                                                            Tang
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The present invention relates to phosphatase polypeptides, nucleotide sequences encoding them, as well as various products and methods useful for the diagnosis and treatment of various phosphatase-related diseases and conditions. Substance that modulates the activity of phosphatase conditions. Substance that modulates the activity of phosphatase and conditions. Substance that modulates the activity of phosphatase collapsed is used to treat immune-related diseases and disorders, including cancers of tissues, cancers of nematopoletic origin, diseases of central and peripheral nervous system, Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, viral: infections, infections caused by prions, bacteria and fungi, ocular diseases, diabetes, myradines, pain, secural dysfunction, modo disorders, attention disorders, nypotension, hypertension, psychotic disorders, neurological disorders, dyskinesias and organ transplant rejection. The present amino acid sequence is classified as dual specificity phosphatase (DSP) and MAP chine or the present chine chine the present chine chine the properties or the present chine chi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel phosphatase polypeptide useful for treating cancers, immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases and metabolic disorders
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Pred. No. 0.00053;
); Mismatches 0;
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                                                                               61..204
/label- Phosphatase_domain
1..173
/label- Catalytic_domain
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99US-0175766.
2000US-0178078.
2000US-0179301.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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N-PSDB; AAD09497.
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Best Local Similarity
Matches 12; Conserv
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28-DEC-1999;
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Flanagan P;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New cardiovascular system associated protein tyrosine phosphatases are used in the diagnosis and treatment of e.g. immune disorders, anti-proliferative disorders, metabolic disorders and cardiovascular
                                                                                                                                                                                                                                                                                                                      /note= "Protein himss" - .
223..225
/note= "Protein Kinase C phosphorylation site"
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te= "Protein Kinase C phosphorylation site"
                                                                                                   "Protein Kinase C phosphorylation site"
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                                                                                                                                   note= "tyrosine kinase phosphorylation site"
                                                                                                                                                                                  /note- "phosphatase catalytic active domain" 89..92
                                                                                                                     "helix-loop-helix DNA binding domain"
hypotensive; cardiant; tyrosine phosphatase modulator.
                                                                                                                                                                                                                                                                 "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                ..251
te= "N-myristoylation site"
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                                          ...131
/label= N_terminal_domain
/note= "unique"
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176..179
^^te= "amidation site"
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                                     Location/Qualifiers
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                   Homo sapiens
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a neural disorder, a cardiovascular disorder e.g. hypertension or coronary heart disease or a disorder rising from improper phosphorylation of a phosphorylated protein. Anti-CSAPTP antibodies are used to isolate CSAPTP by standard techniques, to facilitate the purification of natural and recombinantly produced CSAPTP from cells, to detect CSAPTP protein in cell supernatant for evaluating the level of CSAPTP expression and to monitor protein levels in tissue as part of a cilnical testing procedure to determine efficacy of a treatment procedure. CSAPTP nucleic acids, antibodies and protein molecules can be used in screening assays and in predictive medicine e.g. prognostic assays, monitoring clinical trials
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine.
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100.0%; Pred. No. 0.00065;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                               and pharmacogenetics.
                                                                                                                                                                                                                                                                                                                                263 AA;
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MKP; migraine; chromosome 10q21.3.

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Homo sapiens
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28-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel genes (AAI62752-AAI62961) and proteins (AAM42347-AAM42415) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adream gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. addison's disease, allergies, autoimmune hamolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel plasma membrane associated proteins useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancer, immune response and neuronal disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; SEQ ID NO 88; 532pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human SGP014 phosphatase polypeptide.
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                   05-DEC-2000; 2000US-0251988.
05-DEC-2000; 2000US-0256719.
06-DEC-2000; 2000US-0251479.
08-DEC-2000; 2000US-0251999.
11-DEC-2000; 2000US-0254097.
                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
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nes 12; Conserv
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The present invention relates to phosphatase polypeptides, nucleotide sequences encoding them, as well as various products and methods useful for the diagnosis and treatment of various phosphatase-related diseases and conditions. Substance that modulates the activity of phosphatase polypeptide is used to treat immune-related diseases and disorders, including cancers of tissues, carcitovascular disease, brain or neuronal-associated diseases and metabolic disorders, including cancers of tissues, cancers of hematopoletic origin, diseases of central and peripheral nervous system, Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic. Lateral sclerosis, viral infections, infections caused by prions, bacteria and fungi, ocular diseases, diabetes, migraines, pain, saxual dysfunction, mood disorders, attention disorders, ognittion disorders, hypotension, hypertension, psychotic disorders, neurological disorders, dyskinesias and organ transplant rejection. The present anno acid sequence is human ScPO14 phosphatase polypeptide. This sequence is classified as dual specificity phosphatase (DSP) and MAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel phosphatase polypeptide useful for treating cancers, immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases and metabolic disorders
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                                                                                              37..181
/label- Phosphatase_domain
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                                                              /label= Catalytic_domain
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Location/Qualifiers
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99US-0175766.
2000US-0178078.
2000US-0179301.
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ses 12; Conservative
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N-PSDB; AAD09496.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SUGE-) SUGEN INC.
                                                                                                                                                                                                                                               WO200146394-A2
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## GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

February 8, 2002, 15:45:01 ; Search time 15.43 Seconds
(without alignments)
1086.092 Million cell updates/sec

US-09-847-519A-2

Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

219241 seqs, 76174552 residues Searched: Word size :

0 Total number of hits satisfying chosen parameters:

Post-processing: Listing first 1000 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Database :

PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description esult No. Score Match Length DB ID n to a

No matches found

Result

Search completed: February 8, 2002, 15:48:10 Job time: 189 sec

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## GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

February 8, 2002, 15:46:07 ; Search time 11.72 Seconds (without alignments) 688.248 Million cell updates/sec

US-09-847-519A-2
220
1 MTSGEVKTSLKNAYSSAKRL.....VQQRRRSQRQDGEEEDGREL 220

OLIGO Gapop 60.0', Gapext 60.0 Title: Perfect score: Sequence: Scoring table:

100059 seqs, 36664827 residues

Searched:

10

Word size :

0 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

esult Query No. Score Match Length DB Result

Description

No matches found

Search completed: February 8, 2002, 15:49:20 Job time: 193 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein – protein search, using sw model
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February 8, 2002, 15:45:47; Search time 23.66 Seconds Run on:

(without alignments) 1360.098 Million cell updates/sec

US-09-847-519A-2

Perfect score:

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1 MTSGEVKTSLKNAYSSAKRL......VQQRRRSQRQDGEEEDGREL 220 Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

473505 seqs, 146272329 residues

Searched:

10 Word size : Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 ... Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

SPTREMBL\_17:\* Database :

sp\_archea:\* sp\_bacteria:\* sp\_fungi:\*

sp\_human:\*
sp\_invertebrate:\*
sp\_mammal:\* sp\_organelle:\* sp\_phage:\* sp\_rodent:\* sp\_plant: \* sp\_virus:\* sb\_mhc:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_unclassified:\*

sp\_vertebrate:\*

## SUMMARIES

	O9btwo homo sapien O9d700 mus musculu O9bv47 homo sapien
ption	homo homo
Description	09btw0 09d70 09d70
	O9btw0 homo sapie Q9d700 mus muscu Q9bv47 homo sapie
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DB	4 11 4
Query Match Length DB ID	86 198 211
Query	
Score	122
Result No.	357

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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
UNKNOWN (FROTEIN PR MGC:2627).
HOMO Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                            86 AA
ALIGNMENTS
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                                                                            PRELIMINARY;
                                                                       Q9BTW0
Q9BTW0;
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Q9BTW0
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Gaps

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Indels

Length 198;

DB 11; I

5.5%; Score 12; DB 100.0%; Pred. No. 0.0.1ive 0; Mismatches

Query Match 5.5 Best Local Similarity 100. Matches 12; Conservative

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RA Kawai J. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishili Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arawawa T., Iawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Rosole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubi F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Blake J., Boffelli D., Bojunga N., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustinotch S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Machara I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Haysahizasi Y., Stohleisuki S.,
RA Haysahizasi Y., Rawai Y., Kawai H., Kohtsuki S.,
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                         ;
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                                                                             Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003115; AAH03115.1; -.
SEQUENCE 86 AA: 9652 MW; 4DD29AFD5989528B CRC64;
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Last annotation update)
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0.00017;
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                                                                                                                                                                                             Score 12;
Pred. No.
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SMART; SM00012; PTPc_DSPc; 1.
PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
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EMBL; AKO09781; BAB26501.1; -

MGD; MGI:1914209; 2310043K02Rik.

InterPro; IPR000340; DS_phosphatase.

InterPro; IPR000387; TYR_phosphatase.

Pfam; PF00782; DSPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN 2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-TONGUE;
MEDLINE-21085660; Pubmed-11217851;
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                                                                                                                                                                                             Query Match 5.5%; Soc
Best Local Similarity 100.0%; Pr
Matches 12; Conservative 0;
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                                                                                                                                                                                                                                                                               152 SRSATLVLAYLM 163
                                   SEQUENCE FROM N.A. TISSUE=NEURÓBLASTOMA;
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                                                                                                                                                                                                                                                                                                      32 SRSATLVLAYLM 43
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NCBI_TaxID=9606;
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SEQUENCE
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OBBV47:
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:1136).
Homo sapiens (Human).
Homo sapiens (H
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TISSUB-LUNG CARCINOMA;
Strausborg R.;
Submitted (AAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC001613; AAH01613.1; -.
SEQUENCE 211 AA; 23945 MW; 60E944304905086D CRC64;
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Search completed: February 8, 2002, 15:49:02 Job time: 195 sec

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Sequence Sequence

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6268135el Phospholipase Molecule and Uses Therefor
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Pred. No. 1.1e-36;
0; Mismatches 166;
                                                                US-08-869-696-20
US-08-387-942C-19
US-08-387-942C-19
US-08-869-696-21
US-08-869-696-22
US-08-869-696-8
US-08-869-696-8
US-08-81-742-1
US-08-951-742-1
US-08-951-742-1
US-08-9696-1
US-08-969-1
US-08-969-1
US-08-91-747A-4
US-09-130-114-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09163833
Patent No. 6268135
GENERAL INFORMATION:
TITLE OF INVENTION: No. 6268135el Phospholipp FILE REFERENCE: mni-059
CURRENT APPLICATION NUMBER: US/09/163,833
CURRENT APPLICATION NUMBER: US/09/163,833
CURRENT FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
SEG ID NOS: 580 
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Best Local Similarity 64.3%;
Matches 299; Conservative
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ORGANISM: Homo sapiens
FEATURE:
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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Compugen Ltd.
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US-09-113-881-12
US-09-164-193-6
US-07-988-273-1
US-08-30-290-11
US-08-30-290-11
US-08-990-379-2
US-08-990-379-2
US-08-941-445A-10
US-08-941-443-14
US-08-199-5
US-08-528-199-5
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                GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Perfect score:
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Maximum DB s
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Pred. No. 5.1e-31;
0; Mismatches 165; Indels
                                                                                           APFLICANT: Shaĥ, Purvi
TTLE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                       Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF-0470 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: BILLINGS, LUCY J. REGISTRATION NUMBER: 36,749
Bandman, Olga
Lal, Preeti
Hillman, Jennifer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 63.0%;
Matches 312; Conservative (
                                                                                                                                                                                     3174 Porter Drive
                                                      Corley, Neil C.
Guegler, Karl J.
                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: HEREWITH CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            650-845-4166
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIBRARY: MUSCNOT02;
CLONE: 971204
US-09-013-881-12
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APPLICANT:
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APPLICANT: Acton, Susan
TITLE OF INVENTION: No. 6268135el Phospholipase Molecule and Uses Therefor
TITLE OF INVENTION: No. 6268135el Phospholipase Molecule and Uses Therefor
CURRENT APPLICATION NUMBER: US/09/163,833
CURRENT FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
                   181 aaccatatcgatgaggtctggcccagcctcttcctgggagatgcgtacgcagcccgggac 240
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gocatocagoaagtggccaagaaccgctgcgtcctcccgaaccggggctttttgaagcag
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Pred. No. 1.2e-36;
0; Mismatches 166;
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Patent No. 6132964
GENERAL INFORMATION:
                                                                                                                                                                                                         Sequence 1, Application US/09163833 Patent No. 6268135
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Best Local Similarity 64.3%;
Matches 299; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: CDS
; LOCATION: (52)..(645)
US-09-163-833-1
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US-09-013-881-12
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                                                                                                                                                                    RESULT 2
US-09-163-833-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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GENERAL INFORMATION:

APPLICANT: Acton, Susan L.

APPLICANT: Acton, Susan L.

TITLE OF INVENTION: NOVEL CSAPTP NUCLEIC ACID MOLECULES AND USES THEREFOR (as ame FILE REFERENCE: MII-051

CURRENT PEPLICATION NUMBER: US/09/164,193C

CURRENT FILING DATE: 1998-09-30

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PATENTIN Ver: 2.0

SEQ ID NO 4

LENGTH: 1016
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Patent No. 5512434
GENERAL INFORMATION:
APPLICANT: BATENOSON, Stuart A.
APPLICANT: BOTTARO, Donald P.
APPLICANT: MIKI, Toru
TITLE OF INVENTION: EXPRESSION CLONING OF A HUMAN
TITLE OF INVENTION: PHOSPHATASE
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                      DB 4;
                                                                                                                                                                                                                                                                                                                                                    Query Match 13.9%; Score 161.6; DB 4; Best Local Similarity 61.9%; Pred. No. 4.8e-28; Matches 276; Conservative 0; Mismatches 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                665 cgtcctcccgaaccggggcttttga 690
                                             Sequence 4, Application US/09164193C Patent No. 6258582
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                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                          ; LOCATION: (1)..(789)
US-09-164-193-4
                                                                                                                                                                                                                                                                          NAME/KEY: CDS
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                               JS-09-164-193-4
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TITLE OF INVENTION: NOVEL CSAPTP NUCLEIC ACID MOLECULES AND USES THEREFOR (as amended CURRENT APPLICATION NUMBER: US/09/164,193C
CURRENT FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 2.0
SOFTWARE: Patentin Ver. 2.0
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                                                                                       CAGCCAGGAGGGAAGATCCTGGTGCATTGTGCTGTGGGCGTGAGCCGATCCGCCACCCTG 885
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Pred. No. 4.5e-28;
); Mismatches 164; Indels 6
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US-09-164-193-6
Sequence 6, Application US/09164193C;
Patent No. 6298582;
GENERAL INFORMATION:
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ilarity 61.9%;
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                                                                                                                                                   711 aagcagctggtgcag
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; LOCATION: (1)..(789)
US-09-164-193-6
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LENGTH: 789
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Matches 276;
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CLONING OF A HUMAN
                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12019
                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,273
FILING DATE: 14-DEC-1992
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 861 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
Sequence 1, Application PC/TUS9312019
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                   TITLE OF INVENTION: EXPR
TITLE OF INVENTION: PHOS
NUMBER OF SEQUENCES: 7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 269; Conservative
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                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
PCT-US93-12019-1
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US-08-530-290-11
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Pred. No. 1.4e-21;
0; Mismatches 200; Indels
                                                                                                                                                  SOFTWARE: Paterin Ralease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988,273
CILAGE DATE: 19921214
                                                                                                                                                                                                                                                                                                                           40399/182 NIHD
                 3000 K Street, N.W., Suite 500 Washington, D.C.
                                                                   ZIP: 2000-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40395
TELECOMMUNICATION INFORMATION:
TELERAX: (202)672-5399
TELERAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 861 base pairs
TYPE: NUCLEIC ACID
STRANDENESS: double
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56.6%;
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Matches 269; Conservative
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 ADDRESSEE:
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; LOCATION:
US-07-988-273-1
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263 cagicoccagitacacccacgicaacgaggiciggcccaagcictacaiiggcgaigaggc 322
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                                                                                                                                                                                                                                                                                    217 TGAGGGCAGGTCCTTCATGCACGTCAACACCCAACTTCTACAAGGACTCCGGCAT 276
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                                                                         0; Mismatches 200; Indels
11.4%; Score 133; DB 5; 56.6%; Pred. No. 1.4e-21;
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Patent No. 5958721
GENERAL INFORMATION:
APPLICANT: Marshall, Christopher John
APPLICANT: Ashworth, Alan
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RESULT 7 PCT-US93-12019-1

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GENERAL INFORMATION:
APPLICANT: SCOR', Philip J
APPLICANT: STOR', Philip J
APPLICANT: STOR', Philip J
APPLICANT: MISTA-Press, Anita
APPLICANT: MISTA-Press, Anita
TITLE OF INVENTION: Their Biologically Active Expression Products
TITLE OF INVENTION: Their Biologically Active Expression Products
TITLE OF INVENTION: Their Biologically Active Expression Products
FILE REPERENCE: 4104-0003228A
FILE REPERENCE: 1997-12-15
CURRENT APPLICATION NUMBER: PCT/US96/10402
EARLIER PELLING DATE: 1995-06-14
EARLIER FILING DATE: 1995-06-16
SOFTWARE: PATCHIN VOIT: 2.0
SOFTWARE: PATCHIN VOIT: 2.0
SOFTWARE: PATCHIN VOIT: 2.0
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Patent No. 5998188

GENERAL INFORMATION:
APPLICANT: Stock, Philip J
APPLICANT: Misra-Press, Anita
TITLE OF INVENTION: Misse: 1090122018A
CURRENT APPLICATION NUMBER: US/08/990,379
CURRENT FILING DATE: 1997-12-15
EARLIER APPLICATION NUMBER: PCT/US96/10402
EARLIER PILING DATE: 1996-06-14
EARLIER FILING DATE: 1995-06-16
NUMBER OF SEQ ID NOS: 19
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                                                                                                     Sequence 1, Application US/08990379 Patent No. 5998188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.2%;
Best.Local Similarity 51.1%;
Matches 168; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Rattus norvegicus
US-08-990-379-1
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                                                                              US-08-990-379-1
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APPLICANT: Hughes, David Anthony
TITLE OF INVENTION: Methods for Screening of Substances for
TITLE OF INVENTION: Therapeutic Activity and Yeast for Use Therein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3;
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Best Local Similarity 52.9%; Pred. No. 2.3e-07;
Matches 176; Conservative 0; Mismatches 154; Indels
                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA.
                                                                      NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774

REFERENCE/DOCKET NUMBER: 084611-000000US
TELEFONMUNICATION INFORMATION:
TELEFONG: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SED ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1238 base pairs
TYPE: nucleic acid
STRANDENNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRILING DATE: 31-MAR-1994
PRIOR APPLICATION NUMBER: WO PCT/GB94/00694
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9402573.1
FILING DATE: 10-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9307250.2
FILING DATE: 07-APR-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/530,290
FILING DATE: 14-DEC-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 14 CLASSIFICATION:
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US-08-530-290-11
                                                                                                                                                                                                                       COUNTRY:
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INFORMATION FOR SEQ ID NO:
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                                                                                              STRANDEDNESS:
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                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                      395 gaacgiggacacigggcccgactaccgcgacaiggacaiccagtaccacggcgigga 454
                                                                                                                                                            Length 1993
                                                                                                                                                                                                 Indels
                                                                                                                                                        Score 60.2; DB 2;
Pred. No. 6.2e-05;
0; Mismatches 158;
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APPLICANT: SEED, BRIAN
APPLICANT: HAAS, JUKGEN
TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRASESC for Windows Version 2.0
CURRENT APPLICATION DATA::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  00786/345001
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20-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-717-294-42; Sequence 42, Application US/08717294; Patent No. 6114148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 0078
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEPHONE: 617-428-0200
                                                                                                                                                        5.2%;
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                                                       TYPE: DNA
CRGANISM: Rattus norvegicus
US-08-990-379-2
                                                                                                                                                                                               Matches 168; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
SOFTWARE: Patentin Ver.
                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02110
                                     LENGTH: 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                  SEQ ID NO 2
                                                                                                                                                            Query Match
                                                                                                                                                                               Best Local
                                                                                                                                                                                                                                                                                                                 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 GCTACTACCTGGGCGCCCGTGGAGCTGTCCTGGGACTACATGCAGAGCGACCTGGGCGAGC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       274 CGCGCCCCCCTGGATGGGCCTGCTGGGGCCCCACCATCCAGGCCGAGGTGTACGACACCG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tggtggacgccatccagcaagtggccaagaaccgctgcgtcctcccgaaccggggctttt 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        334 TGGTGATCACCCTGAAGAACATGGCCAGCCACCCCGTCAGCCTGCACGCCGTGGGCGTGA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   394 GCTACTGGAAGGCCAGGGGGCGCCGAGTACGACGACCAGACGTCCCAGCGCGAGAAGG 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                           93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 CGCTGGCCACCTTGTACCTGCTGGGGATGCTGGTCGCTTCCGTGCTAGCCGCCACCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               448 gcgtggaggccgacgacctgcccaccttcgacctcagtgtcttctacccggcggcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 TCCCCGTGGACGCCCGCTTCCCCCCCGCGTGCTGCTTCCCCTTCAACAGCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 568 gccgcagccggtcagccaccctggtcctggcctacctgatgatccacaaggacatgaccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 688 tgaagcagctccgggagctggacaagcagctggtgcagcagaggggacggtcccagcgc
                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                          Length 4451;
                                                                                                                                                                                                                                                                                    Score 51.6; DB 3; Length 4 Pred. No. 0.0072; O; Mismatches 239; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Greenlee, Winner and Sullivan, P.C. 5370 Manhattan Circle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Starch Encapsulation
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; Sequence 10, Application US/08941445A
; Patent No. 6107060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
42:
                                                                                                                                                                                                                                                                                       4.48;
                                                     LENGTH: 4451 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Keeling, Peter
APPLICANT: Guan, Hanping
TITLE OF INVENTION: Starcl
                                                                                                                                                                                                                                                                                    Query Match 4.4
Best Local Similarity 44.9
Matches 195; Conservative
                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            748 aggacggtgaggag 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  454 AGGACGACAAGGTG 467
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                                                                                                                                                                      ; MOLECULE TYPE: CDNA
US-08-717-294-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                 linear
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375 aacgeggeecaeggeegetggaaegtggaeatgggeeegaetaetaeegegaeatggae 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      555 cactgogtcatgggccgcagccggtcagccacctggtcctggcctacctgatgatccac 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   673 CAGCGGGGTCTGGAGGACCTCGCGTGCCAACATCCTGATCGACGGGGGGGCGTAC 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       493 AGCGTGGCCCACGACAACGGCCTCGACGGCTTCGTCGCCGACTACCTGGTCGACAGCGTG 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         435 atccagtaccacggcgtggaggccgacgacctccacctcgacctcagtgtcttcttc 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          615 aaggacatgaccctggtggacgccatccagcaagtggccaagaaccgctgcgtcc 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    733 TACGACAACGCCGCGAAGGCGTGCTGCTCAAGATGACCAGCGACATCACCCTGC 787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 4.2%; Score 48.6; DB 2; Length 1 Best Local Similarity 47.8%; Pred. No. 0.023; Matches 141; Conservative 0; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:

APPLICANT: ERTESVAG, HELGA
APPLICANT: VALLA, SVEIN
APPLICANT: SKJAK-BRAEK, GUDMUND
APPLICANT: SKJAK-BRAEK, GUDMUND
APPLICANT: LARSEN, BOORN
TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES
TITLE OF INVENTION: ENCODING MANNURONAN C-5-EPIMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP STREET: P.O.BOX 747
CITY: FALLS CHURCH
                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,942C
FILING DATE: 09-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08387942C Patent No. 5939289
                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M.
REGISTRATION NUMBER: 28,977
REFERENCE/CDCKET NUMBER: 1809
TELECOMMUNICATION INFORMATION:
TELEPHONE: 702-205-8000
TELEPHONE: 703-205-8050
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1176 base pairs
                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22042
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US-08-387-942C-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1395 GAGCGAGTGGAACCCCGCTGTGGACGTGCACCTCCGACGACGACTACACCAACTACAC 1454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1515 CCTGCAGGTCCGCGACGACGTGCCACTGATCGGGTTCATCGGGCGGCGGTGGACCACCAGAA 1574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1575 GGGCGTGGACATCATCGCCGACGCGATCCACTGGATCGCGGGCGAGGACGTGCAGCTCGT 1634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            422 ccgcgacatggacatccagtaccacggcgtggaggccgacgacctgcccaccttcgacct 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               482 cagigiciticitateceggeggeagecticategaeagagegetaagegaegaeeaeag 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          602 cctgatgatccacaaggacatgacctggtggacgccatccagcaagtggccaagaaccg 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             662 ctgcgtcctcccgaaccggggcttttgaagcagctccgggaagctggacaagcagctggt 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               542 taagatcctggttcactgcgtcatgggccgcagccggtcagccacctggtcctggccta 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2097;
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Patent No. 5939289

GENERAL INFORMATION:
APPLICANT: ERTESVAG, HELGA
APPLICANT: SKJAK-BRAEK, GUDMUND
APPLICANT: SKJAK-BRAEK, GUDMUND
TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES
TITLE OF INVENTION: ENCODING MANNURONAN C-5-EPIMERASE
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: P.O.BOX 747
CITY: FALLS CHURCH
CITY: CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 49.8; DB 3; Length 2
Pred. No. 0.014;
0; Mismatches 162; Indels
PRIOR APPLICATION DATA:
APPLICATION UNDRER:
FILING DATE: 30-SEP-1996
ATTORNEY AGENT INFORMATION:
NAME: Winner, Ellen P
REGISTRATION NUMBER: 89-97
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8089
TELEPHONE: (303) 499-8089
TELEPHONE: (303) 499-8089
TELEPHONE: (303) 499-8089
TELEPHONE: CANACTERISTICS:
EMOTH: 2097 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                    CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 47.6%;
Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                                                     SS: double
not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: 1..2097
US-08-941-445A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1635 GATGCTGGG 1643
                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: not re
MOLECULE TYPE: CDN
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 722 gcagcagag 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-387-942C-17
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NAME/KEY: CDS
LOCATION: 744..11219
OTHER INFORMATION: /function= "gene= "eryA""
OTHER INFORMATION: /product= ""ORF1 encoding modules 1 & 2 for OTHER INFORMATION: 6-deoxyerythronolide B""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: 2250.3626
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylACP synthase domain/module1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LCCATION: 744..1868
CTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain 1 of module 1"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 3831..4811
OCHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase 2 domain of module 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 1998..2198
OTHER INFORMATION: /function= "approximate span of
PERTINFORMATION: acyl carrier domain 1 of module
FEATURE:
                                                   ADDRESSEE: Edward H. Gorman
STREET: Abbott Laboratories D377/AP6D-2 One Abbott
STREET: Park Rd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: /function= "APPROXIMATE SPAN OF OTHER INFORMATION: /label= FUNCTION
                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CUBRENT APPLICATION DATA:
PLICATION NUMBER: US/07/642,734C
FILING DATE: 17-JAN-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Saccharopolyspora erythraea
STRAIN: NRRL 2338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 4952.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-9396
TELEFAX: 708-938-2623
                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                         COUNTRI, ...
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPatible
                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 17-JAN-91
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Danckers, Andreas M
REGISTRATION NUMBER: 32652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 11219 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 744..6659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
                                                   CORRESPONDENCE ADDRESS
                                                                                                                                       Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: N
ANTI-SENSE: NO
ORIGINAL SOURCE:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1022 TACGACAACGCCCGCGAAGGCGTGCTCCAAGATGACCACGGACATCACCTGC 1076
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APPLICANT: Katz, L
APPLICANT: Donadio.
APPLICANT: Macabine, J B
TITLE OF INVENTION: Recombinant DNA Method for Producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 48.6; DB 2; Length 1
Pred. No. 0.048;
0; Mismatches 154; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/387,942C
FILIG DATE: 09-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE: ORGANISM: Azotobacter vinelandii
                                                                                                              FILING LASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1809
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8050
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 12588 base pairs
TYPE: nucleic acid
"""""" TYPE: nucleic acid
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Best Local Similarity 47.8%;
Matches 141; Conservative
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6702..9695
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9973..12588
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2227..6438
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290..1951
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US-08-387-942C-1
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45.9%; Pred. No. 0.057;
tive 0; Mismatches 193; Indels 0;
/function= "approximate span of
beta-ketoreductase domain of module 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
COGATION: 9906..10454
COTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoreductase domain of module 2"
                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 6678.8066
OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: beta-ketoacyl ACPSynthase of module 2"
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LOCATION: 8262..9305
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain of module 2"
                                                           NAME/KEY: misc_feature
LOCATION: 6369..6626
OTHER INFORMATION: /function- "approximate span of
OTHER INFORMATION: acyl carrier domain 2 of module 1"
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LOCATION: 6678..11219
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Matches 164; Conservative
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Run

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Contact: Smith TPL
Contact: Smith TPL
Contact: Smith TPL
Contact: US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Email: Smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904-e. Vector identified by cross_match with the -minscore 18
PCR PRIMERS
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1 (bases 1 to 572)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett Perten, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Perten, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
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221711 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
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AUTHORS
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; Search time 1166.24 Seconds (without alignments) 10734.353 Million cell updates/sec
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Compugen Ltd.
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Copyright (c) 1993 - 2000
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Maximum DB :
                                                                          nucleic
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No.
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FORWARD: AGGAAACAGCTATGACCAT BACKWARD: GTTTTCCCAGTCACGACG Plate: 80 row: I column: 23

FEATURES

500;

56

g ò g ò qq à g ò g ò QQ ò g ò g ò g õ

98 19 146 206

266 238 326 298 386 358 446

Best Loca Matches

Query Match

BASE COUNT ORIGIN

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kidney, lung
                                                                                                                                                                                                                                                                                                                                                                                                   Site_2:
                                                                Rat
                                                                                                                                                                                                                                                                                                                       /clone_lib="Rat gene index, normalized rat, norvegicus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                (REST) Catalog &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GGTTTAGTGTAAGGCTGCCACACCCTTCAGACTGGTACCTCTTAGCCCAGGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254 ctggaagggcagtccccagtacacccacgtcaacgaggtctggcccaagctctacattgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chandra, I., Mason, T.M., Quackenbush, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ggctgggcgtgcggctgctacatgcccacggaccagaacctcccgacgcggccaggccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 cggcacacccagctgcagaaaggagagaaaatcccttggctctaaaatgacatctggaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 agtgaagacaagcctcaagaatgcctactcatctgccaagaggctgtcgccgaagatgga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   295 TGATGAGGCCACAGGGGGGGGGCTGCAGGGCTGCAGAAGGCCGGCTTCACGCAGGGCT
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                                                                                                                                                                                                   ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 634;
                                                                                                                                                                                                   the
                                                                      General Index (1998)
Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-0208
Email: nhlee@tigr.org
This clone is available through the ATCC, contact the tel#703-555-2700 for further information
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                             liver, embryo, heart, muscle, spleen"
/lab.host="SOLR"
                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pBlueScript SK(-); Site_1:
Xhol; Estimated insert size approx.1 kb"
201 c 181 g 112 t
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                                                                EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 425.8; DB 10;
Pred. No. 8.5e-67;
0; Mismatches 112;
                                                              a Rat
                                                                                                                                                                                                                                                                           norvegicus"
              1 (bases 1 to 634)
Lee,N.H., Glodek,A., Chandra,I., M
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of
                                                                                                                                                                                                                                                                                      /db_xref="taxon:10116"
/clone="RGIES16"
                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                         /organism="Rattus
                                                                                                                                                                                                                                                                                                                                       Bento Soares"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.5%;
llarity 81.4%;
Conservative
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520; Conserv
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    Rattus
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Matches
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                 REFERENCE
                                 AUTHORS
                                                                                                                                                                                                                                             FEATURES
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ORIGIN
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                  /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas,
                                                                                                                                                                                                                                                                                                                                                                                                                               202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           177
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                                                                                                                                                                                                                                                                                                                                                                                                                                          121 CCTCAAGAACGTCTACCCATCTGCCAAGAAGCTGCTGCCGAAGGTGGAGGAG---GGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cggccgctggaacgtggacactgggcccgactactaccgcgacatggacatccagtacca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ggctgctacatgccccacggaccagaacctcccgacggccaggccccggcacacccag
                                                                                                                                                                                                                                                                                                                                                                                              CTGCAGAAAGGAAAGAAAATCCCTTGGCTCCAAAATGACATCCGGAGAATCGAAGACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                            cctcaagaatgcctactcatctgccaagaggctgtcgccgaagatggaggaggaaggggga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCTGAGGATTACTGTACTCCTGGAGCCTTCGAGCTGGAGCGTCTCTTCTGGAAAGGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
                                                                                                                                                                                                                                          Length 572;
                                                                                                                                                                                1 others
                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                          DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST
                                                                                                                                                                                                                                                     4.1e-70;
ches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AW918423 634 bp mkna
EST349727 Rat gene index, normalized
Rattus norvegicus CDNA clone RGIES16
                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                 66
                                                                                                                                                                                                                                          Score 444.4;
Pred. No. 4.1
                                                                                                                                                              adrenal, and endometrium.
187 c 161 q 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGCCGCAGCCGGTCGGCGACTCTGGTCCTGGCCT
                                          /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC_2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
primer: ATTTAGGTGACACTATAG
              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GI:8084199
                                                                                                                                                                                                                                          38.1%;
87.0%;
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                         1. .572
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AW918423.1
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EST

VERSION KEYWORDS SOURCE ORGANISM

DEFINITION

RESULT AW918423

ACCESSION

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                                                                                                                                                  AW918455 605 bp mRNA EST 25-MAY-2000 EST349759 Rat gene index, normalized rat, norvegicus, Bento Soares Rattus norvegicus cDNA clone RGIES53 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="mix - brain, ovary, placenta, kidney, lung,
liver, embryo, heart, muscle, spleen"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pBlueScript SK(-); Site_1: EcoRl; Site_2:
Xhol; Estimated insert size approx.1 kb"
192 c 173 g 106 t
                                                                                                                                                                                                                                                                            Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                           Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Rat gene index, normalized rat, norvegicus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 agigaagacaagccicaagaaigcciacicaicigccaagaggcigicgccgaagaigga 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 CACAAAGACAAGCGTCAAGCATGCCCACCTGTGCCGAGAGGTTGTCCCTGCA---GCA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ggaggaagggaggaggactactgcaccctggagcctttgagctggagcggctctt 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 605)
Lee, N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog &
This clone is available through the ATCC, contact the ATCC tel#703-365-2700 for further information Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
TTE1: (301)-838-3529
Fax: (301)-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 401; DB 10; Length 6
Pred. No. 2.4e-62;
0; Mismatches 110; Indels
                                             /organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="RGIES53"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1. 605
                                                                                                                                                                                                               AW918455.1 GI:8084231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bento Soares"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: nhlee@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 34.4%;
Best Local Similarity 80.9%;
Matches 494; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1998)
                                                                                                                                                                                                                                                              norvegicus
                                                                                                                                                                                                                                               Norway rat
                                                                                                                                                                                                                                                                                                                                                                                        Gene Index
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                                                                                                                                                                                                                                                               Rattus
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ORIGIN
                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                            ORGANISM
                535
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COMMENT
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AW918455
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SOURCE
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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovoidea; Bovoidea; Bovoidea; Bovoidea; Bovoidea; Boxoina; L. (bases 1 to 278) Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Keele, J.W.
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/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from marrow, alveolar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence evaluation of four pooled-tissue normalized bovine cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                               534
235 CTGGAAGGCAGCCCCCAGTACACACACGTCATGAGGTCTGGCCTCGGCTCCATGTTGG 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-APR-2001
                                                                                                                                                                                475 CTACTCGGCTGCCGCCTTCATCGACTCGGCGCTCCAAGACGACCACAGTAAGATCCTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BF652341 478 bp mRNA EST 2
275868 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
BF652341
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Fax: 402 762 4390
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Plate: 65 row: K column: 11
Seq primer: ATTTAGGTGACACTATAG.
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/clone_lib="MARC 3BOV'
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett
G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
macrophage, ovary, fetal semitendonosus muscle, and fetal
longissimus muscle."
1 152 c 134 g 84 t
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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                                                                                                                                                                            cgactactaccgcgacatggacatccagtaccacggcgtggaggccgacgacctgcccac 472
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                                                                                                    Gaps
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                                                                                                    3;
                                                                           Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE808287 505 bp mRNA EST 2
213454 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
BE808287 GI:10239399
                                                                                                    60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4360
Fax: 402 762 4390
                                                                         Score 368; DB 11;
Pred. No. 2.1e-56;
0; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: smith@email.marc.usda.gov
                                                                        31.6%;
86.9%;
                                                                                     Best Local Similarity 86.9
Matches 417; Conservative
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COMMENT
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AUTHORS
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LOCUS

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Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
                                                                                                                                                                                                                                                                    /note="Vector: pCMV SPORT6; Site_1: Xba1; Site_2: Xho1; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."

145 c 163 g 84 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 505;
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BF430044.1 GI:11442141
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                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 242.4; DB 11;
Pred. No. 6.1e-34;
0; Mismatches 116;
and -minmatch 12 options.
PCR PRIMETS
FORWARD: AGGAAACAGCTATCACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 67 row: P column: 14
Seq primer: ATTTAGGTGACGTATAG.
                                                                                                                                                                                  /db_xref="taxon.9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                   /organism="Bos taurus"
                                                                                                                           Location/Qualifiers
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Best Local Similarity 73.3%;
Matches 356; Conservative
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/clone_lib="Nii_MGC_19"
/tissue_type="neuroblastoma"
/lab_host="bH10B (phage-resistant)"
/note="Organ: brain: Vector: porB7; Site_1: XhoI; Site_2:
EcoR1; cDNA made by oligo-dr priming. Directionally
cloned into EcoR1/XhoI sites using the following 5'
adaptor: GGCACGAGG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (university of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NI_MGC Library."
                                                                                                                                                                                                                                                                                                                                       L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capabs-rement: All of the Contact 
                                                                                                                                                                                              Eukaryota Metazoa; Chordata; Cranlata; Vertebrata; Euteleostoml; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 703)
NIH-MGC http://mgc.nci.nih.gov/.
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602761093F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4896479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                471 accttcgacctcagtgtcttcttctacccggcggcagccttcatcgacagagcgctaagc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4896479"
                                                                                      BI199835.1 GI:14654856
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59.6%;
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                                   mRNA sequence.
                                                                                                                                                                            Homo sapiens
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                                                           ACCESSION
                                                                                         VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: Uni-ZAP.XR; Site_1: EcoRI; Site_2: XhoI; Library obtained from Stratagene, catalog #937721. Library ande from skeletal muscle of a two year old Holstein cow." 147 c 136 g 107 t
                                               Marken, W.C., Tao.N., Allison, T., Wagner, S., Mathialagan, N., Kata, S., Johnson, J., Smith, T.P.L. and Womack, J. Mathialagan, N., Kata, S., Johnson, J., Smith, T.P.L. and Womack, J. Genes transcribed in bovine skeletal muscle Unpublished (2000) Contact: Smith TPL Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Fax: 402 762 4390
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                                                                                                                                                                                                                                                                                                                                       Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore and -minmatch 12 options.

PCR PRIMERS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 AGCCCGGGACAAGAACAAGTTGACCCAGCTGGGCATCACACATGTTGTGAATGTTGCCGC 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cggccgctggaacgtggacactgggcccgactactaccgcgacatggacatccagtacca 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     626 cctggtggacgccatccagcaagtggccaagaaccgctgcgtcctcccgaaccgggctt 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTGGTGGAGGCCATCCAGACAGTGCAAGCCCACCGCGATATCTGCCCCCAACTCGGGCTT 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 AGGCAAGTITCAGGTGGACACAGGTGCCAAGTTCTACCGCGGAATGCCCTTGGAGTACTA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 2.4e-26;
0; Mismatches 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="MARC BSM"
/tissue_type="Skeletal muscle"
/lab_host="XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     FORWARD: GGAAACAGCTATGACCATG
BACKWARD: GTTTTCCCAGTCACGAC
Seq primer: AATTAACCCTCACTAAAGGG.
                                                                                                                                                                                                                                                                                                               Email: smith@email.marc.usda.gov

    .486
    /organism="Bos taurus"

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  idae; Bovinae; Bos. (bases 1 to 486)
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Best Local Similarity 64.4%;
Matches 299; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
5 (bases 1 to 1748)
5 (bases 1 to 1748)
6 Alaawa, T., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imochani, K., Ishii, Y., Itoh, M., Izawa, M., Kato, H., Kawai, J., Kolima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genes
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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AK009781
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                                                    391 GTACTGGCCTACCTCATGCTGTACCACCATCCTTACCCTCGTGGAGGCCATCAAGAAAGTC 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 (bases 1 to 1748)
The RIKEN Genome Exploration Research Group Phase II Team and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (strain:C57BL/6J) adult male tongue cDNA to mRNA clone_lib:RIKEN full-length enriched mouse cDNA library
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                                                                                                        451 AAAGACCACCGAGGCATCATCCCCAACCGGGGCTTCCTGAGGCAGCTCCTGGCCCTGGAC
                                                                                                                                                             711 aagcagctggtgcagcagaggcgacggtcccagggccaggacggtgaggaggatggc
                                                                                                                                                                                                                 511 CGCAGGCTGCGCCAGGGTCTGGAAGCATGAGGGGACGGGGAGGAGGAGGTCAGGCCAGGCCC
                                                                                                                                                                                                                                                                      771 agggagctgtaggcccgactcacagggccagcagaggcacttggggacagagggagag
                                                                                                                                                                                                                                                                                                                        571 GTGGTAGGTCCCTGGCTCCCAGCTGGAGATAGGAGGCCCAGGTGGCAGGTAGCAGGAGG
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Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Methods in enzymology. 303, 19-44 (1999)
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Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' AGGAGAGAGAAGARCTOTTTTTTTTTTTTTVN 3', CDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0 and subtraction to of sequence [5' Second strand cDNA was prepared with the primer adapter of sequence [5' Cond Strand CDNA was prepared with the primer adapter.
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/protein_id="BAB26501.1"
/db_xref="GI-12844790"
/translation="MARFSRGSSRSPVRTRGSLEEMPSVHHPFLANFELERLLYTGKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACNHADEVWPCLYLCDQDMANNRRELRRLGTTHVLMASHNRRGTPPAYEGICIRYLG
VEAHDSPAFDMSIHFQTAADFIHRALSQPGGKILVHCAVGVSRSATLVLAYLMLYHHF
TLVEAIKKVKDHRGITPNRGFLRQLLALDRRLRQGLEA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="tongue"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
                                                                                                                                                                                                    Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp, UKL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254 ctggaagggcagtccccagtacacccacgtcaacgaggtctggcccaagctctacattgg 313
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Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tajima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute
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/db_xref="MGD:MGI:1914209"
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/organism="Homo sapiens"
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                                               16.1%;
llarity 61.7%;
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bos.
1 (bases 1 to 558)
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                             729 CAACGCCTCACACAACAGGTGGCGAGGCACC-----CCCGAGGCCTATGAGGGACTGGG 782
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                                                                             caaggacatgaccttggtggacgccatccagcaagtggccaagaaccgctgcgtcctccc
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 gaacgcggcccacggccgctggaacgtggacactgggcccgactactaccgcgacatgga
                                                              494 ctacccggcggcagccttcatcgacagagcgctaagcgacgaccacagtaagatcctggt
                                                                                                                                                                                      554 tcactgcgtcatgggccgcagccggtcagccaccctggtcctggcctacctgatgatcca
                                                                                                                                                                                                                                                                                                               libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                            BF077053 558 bp mRNA EST 2
226847 MARC 2BOV Bos taurus CDNA 5', mRNA sequence.
BF077053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4360
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence evaluation of four pooled-tissue
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/tissue_type="pooled"
/lab_host="DH10B"
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Seg primer: ATTTAGGTGACACTATAG.
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/db_xref="taxon:9913"
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PCR PRimers
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 990)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999) 5, Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: image.llnl.gov 380 284 500 404 48 GGAGATGCCGAAGCCACGCTTGCCCCAGCGTCCTGGAACTGGAGGAGCTCCTGAGGGCA 107 gcccacggccgctggaacgtggacactgggcccgactaccgcgacatggacatccag 440 344 goggoagecticategacagagegetaagegacgaceacagtaagateetggtteaetge 560 atgaccctggtggacgccatccagcaagtggccaagaaccgctgcgtcctcccgaaccgg 680 465 CTCTCCCTGCGCCAGGCGGTGATCACCGTGAGGGAGCGCCGATGGGTCTTCCCCAACAGA 524 Gaps Sapiens cDNA clone IMAGE:4100947 cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayaby: Fhe L.M. AG. E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can ggggaggaggactactgcaccctggagcctttgagctggagggctcttctggaag gegacggettggaccgctataggetgcagaaggeggggttcacgcacgtgetgaacgcg taccacggcgtggaggccgacgacctcccaccttcgacctcagtgtcttcttctacccg 3, Indels Score 187.6; DB 11; Pred. No. 3.8e-24; O: Mismatches 194; ggctttttgaagcagctccgggagctggacaagc 714 558 Ph.D. GGTTTCCTTCACCAGCTCTGCCGGCTGGACCAGC Plate: LLCM971 row: n column: Contact: Robert Strausberg, Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC High quality sequence stop: { Location/Qualifiers BF207232 990 bp mRNA 601870679F1 NIH\_MGC\_19 Homo

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                  /clone="IMAGE:4100947"
/clone=lib="NIH_MGC_19"
/clone_lib="NIH_MGC_19"
/lab_host="DHIOB (phage-resistant)"
/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2: CoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library."
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Mus musculus (strain:C57BL/6J) 10 day old male pancreas CDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:1810015L05.

Mus musculus

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Musinae; Musinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        099
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64.5%;
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1. Caracass 1 to 1104)

1. Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Arakawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanaqaki, T., Hara, A., Hayatsu, N., Hirancto, K., Hiraoka, T., Hori, F., Inotani, K., Ishi, Y., Itoh, M., Izawa, M., Kato, H., Kawai, J., Kawai, J., Kolda, Y., Kouno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Kojima, Y., Kouno, H., Salaki, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shiraki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, R., Yoshida, K., Yoshida, M., Muramatsu, M. and Hayashizaki, Y. Direct Submission

AL Submitted (10-Jul-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Institute, Hamiligenome-reségsc.iken.go.jp, PR: Http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, PR: Research Group of Physical Ads-503-9216)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shibata, K. Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Shibata, K., Itoh, M., Aizawa, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Warahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. Sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the
                                                                                                                                                                                                 2 (bases 1 to 1104)
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genome research. 10 (10), 1617-1630 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 (bases 1 to 1104)
The RIKEN Genome Exploration Research Group Phase II Team and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5 (bases 1 to 1104)
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Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Methods in enzymology. 303, 19-44 (1999)
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/db_xref="MGD:MGI:1914209"
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1 (bases 1 to 471)

Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Gasas, E., Wary, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                           CDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          normalized bovine cDNA
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                                                                                                                                  Length 1104;
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9
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                                            enriched mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5', mRNA sequence
                                                                                                                                                              Indels
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
T=E1: 402 762 4366
Fax: 402 762 4390
                                                                                                                                  DB 12;
                                                                                                                                 Score 166.2; DB 12;
Pred. No. 1.9e-20;
0; Mismatches 153;
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                          /tissue_type="pancreas"
/clone_lib="RKEN full-length
/dev_stage="10 day old"
177 c 350 g 208 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BF774179 471 bp mRNA
273763 MARC 3BOV Bos taurus cDNA
BF774179.1 GI:12122079
/clone-"1810015L05"
                                                                                                                                 14.3%;
ilarity 63.3%;
Conservative
               /sex="male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gcagctggtgcag 725
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Best Local S
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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.990904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR PRIMERS
PCR PRIMERS
PAGABACACCATAGCCAT
PAGGARACACCAGC
PAGGARACACAGCAG
PAGGARACACAGCAGC
PAGGARACACAGCAGC
PAGGARACACAGCAGC
PAGGARACACAGACACATATAGGGGGGACACATATAGGGGGGACACATATAGG.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 415)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä
                                                                                                                                                                                                                                                                                                     ocoled tissue from marrow, alveolar fetal semitendonosus muscle, and fetal
                                                                                                                                                                                                                                                                                   /note="Vector: pCMV SPORT6; Site_1: Xba1; Site_2: Xho1; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."

1 ongissimus muscle."
1 ongissimus muscle."
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CDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                             Score 165.8; DB 11; Length 471; Pred. No. 3.2e-20;
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/clone_lib="MARC 3B0V"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                             1. .471
/organism="Bos taurus"
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Bento
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EST175343 Infant brain,
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A1372800
A1372800.1 GI:4152666
                                                                                                                                                                                                                                                                                                                                                                                                                           14.2%;
ilarity 65.8%;
Conservative
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Matches 258; Conserv
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Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.M., Kelley, J.C., Liu, L.I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shriley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Dimke, D.P., Feng, D.P., Ferrie, A., Fischer, C., Hastings, G.A., He, W., Hu, J. S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Wel, Y.F., Wing, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wel, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anote—"Vector: BA, MI3-derived, Site_1: HindIII; Site_2:
NotI: The infant brain library, constructed by Bento
Soares, Columbia University, was oligo-(dT) primed and
directionally cloned into an MI3-derived plasmid using
total brain mRNA from a 72-day old human female afflicted
with spinal muscular arrophy.

132 c. 123 g. 71 t.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Infant brain, Bento Soares"
/lab_host="E. coli DH5-alpha"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tch 14.1%; Score 164; DB 10; sal Similarity 63.3%; Pred. No. 7.1e-20; 264; Conservative 0; Mismatches 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: (301)-838-0200
Fax: (301)-838-0208
Email: hgl@tigr.org.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96026280
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Matches
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2 (bases 1 to 1065)
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes 20499374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Oka, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagami, M., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yammura, T., Yasunishi, A., Yoshino, M., Muramatsu, M., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shibate, K. Itoh, M. Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Taswa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN Integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1. (Dases 1 to 1065)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning Methods in enzymology. 303, 19-44 (1999)
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The RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                           Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700022L10, full insert sequence.
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                                                                                                                                                                                    05-JUL-2001
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CAP trapper.

Mus musculus (strain:C57BL/6J) adult male testis cDNA to clone_lib.RIKEN full-length enriched mouse cDNA library
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            /proteIn_id="Bab24480.1"
/da_xxef="d1:12839241"
/translation="MSLQKQEIRRRKIHGAVQVSPYQPPTLASLQRLLWVRRTATLTHINEWPOLICEGATARBKGRLIQLGITHVVNVAAGKFQVDTGAKFYRGTPLEYYGI BADDNPFFDLSVHFLEVARXIRDALNIPRSRVLVHCARGVSRSATIVLAFLMIFENMTLVDATGYQALDVAHRDICPNSGFIRQLQVLDNRLRRETGRL"

3 301 c 290 g 229 t
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                                                                                                                                                                                                                                                                                                                           /tissue_type="testis"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
221. .817
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Encyclopedia Project of Genome Exploration Research Group
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Pred. No. 5.8e-20;
0; Mismatches 214; I
                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/db_xref="MGD:MGI:1351599"
/db_xref="MGD:MGI:1901550"
                                                                                                                                                                                                             /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                              /clone="1700022L10"
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57.7%;
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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                     Chases 1 to 456)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,B., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laggreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
                                                                                                                                                                                                                                                               Chordata, Craniata, Vertebrata, Buteleostomi,
Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001) 21180013
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence evaluation of four pooled-tissue normalized
                                                                                                                                         5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TT-1: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10;
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Pred. No. 1.7e-19;
0; Mismatches 157;
                                                                                                                   BE751020 456 bp mRNA
202721 MARC 2BOV BOS taurus CDNA
BE751020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
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Plate: 42 row: P column: 11
Seq primer: ATTTAGGTGACACTATAG.
                  810
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BE751020.1 GI:10165012
                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chc
Mammalia; Eutheria; Cet
Bovidae; Bovinae; Bos
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Local Similarity 62.7%;
les 269; Conservative
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## ALIGNMENTS

Human; SGP003 phosphatase polypeptide; phosphatase-related disease; immune-related disorder; ocular disease; organ transplant rejection; infection; diabetes; palh; sexual dysfunction; Alzhehamer's disease; metabolic disorder; haematopoletic cancer; mood disorder; cardiant; Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; cardiavascular disease; brain; neuronal-associated disease; dyskineala; attention disorder; cognition disorder; psychotic disorder; cytostatic; neuroprotective; antibatedia; notrophic; cerebroprotective; therapy; neuroprotective; antibaterial; vulnerary; tranquilliser; antibathmatic; hypotensive; immunosuppressive; antipsoriatic; antipsoriatic; analgesic; hypertensive; antigraine; chromosome CHR10; ds. )3 phosphatase polypeptide encoding DNA. andard; DNA; 1262 BP (first entry) 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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/\*tag= a /product= "Human SGP003 phosphatase polypeptide" /transl\_except= (pos:492..494, aa:Leu) Location/Qualifiers 240..902

Human SGP003 phosp DNA encoding a hum Probe #9870 used t Probe #22910 used Human SGP060 phosp Human polynucleoti Human CDNA sEQ ID Human CDNA encodin Human SGP014 phosp

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Human; intracellular phosphorylation regulator; HRIP; stroke; myeloma; neurological disorder: Parkinson's disease; demyelinating disease; meniogitis; developmental disorder; neuromuscular disorder; cancer; myasthenia gravis; cell proliferative disorder; actinic keratosis; arteriosclerosis; aleviaemia; melanoma; bronchlis; autoimmune disorder; inflammatory disorder; Addison's disease; acquired immunodeficiency disease; allergy; diabetes mellitus;
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                                                                                                                                                                                                                                          Azimzai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1212 BP; 284 A; 345 C; 373 G; 210 T; 0 other;
 SS
                                                                                                                                                                                                                                          Baughn MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rheumatoid arthritis, microbial infection and trauma
arthritis; microbial infection; trauma;
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Pred. No. 4.4e-230;
0; Mismatches 25;
                                                                                                                                                                                                                                          Hillman JL,
                                         Location/Qualifiers
172..837
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 91.9%;
Best Local Similarity 97.4%;
Matches 1131; Conservative (
                                                                                                                                                                    99US-0125593.
99US-0135049.
99US-0143188.
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                                                                                                                                                2000WO-US07277
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/product=
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                                                                                                                                                                                                                  (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                          Tang YT,
                                                                                                                                                                                                                                                     Au-Young J;
                                                                                                                                                                                                                                                                         WPI; 2000-602121/57.
P-PSDB; AAB18667.
                                                                                                 WO200055332-A2
                                                                                                                                                                    18-MAR-1999;
20-MAY-1999;
09-JUL-1999;
                      Homo sapiens
                                                                                                                                               17-MAR-2000;
                                                                                                                         21-SEP-2000
rheumatoid
                                                                                                                                                                                                                                          Bandman O,
                                                                                                                                                                                                                                                      Lu DAM,
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The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                Probe #22910 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ctgcagaaaggagaaaatcccttggctctaaaatgacatctggagaagtgaagacaag 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ggaggaggactactgcaccctggagcctttgagctggagcggctcttctggaagggcag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       266 tececagtacaceceacgteaacgaggtetggeecaagetetacattggegatga 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 234;
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                                                 Probe; microarray; human; placenta; antenatal diagnosis;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.1%; Score 234; DB 22;
100.0%; Pred. No. 2.5e-43;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       analyzing gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 25; SEQ ID No 22910; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                            Rank DR;
                                                                                                                                                                                                                                                                                                                                            (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                          Chen W,
                                                                                                                                                                                                                04-FBB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-UNN-2000; 2000US-06084.08
03-AUG-2000; 2000US-053366.
21-SBP-2000; 2000US-0234687.
27-SBP-2000; 2000US-0234687.
04-OCT-2000; 2000GB-0024263
                                                                                                                                                                                                                  ; 2000us-0180312.
; 2000us-0207456.
; 2000us-0608408.
; 2000us-0632366.
; 2000us-0234687.
                                                                                                                                                                                       2001WO-US00663
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Best Local Similarity 100.
Matches 234; Conservative
                                                                 SS.
                                                                                                                                                                                                                                                                                                                                                                         Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-488897/53
                                                                 genetic disorder;
                                                                                                                           WO200157272-A2
                                                                                                Homo sapiens
                                                                                                                                                                                       30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
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   to measure gene expression in human placenta sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful for
analyzing gene expression in human placenta -
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                                Probe; microarray; human; placenta; antenatal diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 556 BP; 115 A; 153 C; 154 G; 134 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 241; DB 22;
Pred. No. 8.6e-45;
0; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 25; SEQ ID No 9870; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                          Rank DR;
                                                                                                                                                                                                                                                                                                                                                         Chen W,
                                                                                                                                                                                                  2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
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                                                                                                                                                                     30-JAN-2001; 2001WO-US00663
                                                                                                                                                                                                                                                                                             04-OCT-2000; 2000GB-0024263
                                                                                                                                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 20.79
Best Local Similarity 89.6
Matches 259; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA;
                                                genetic disorder; ss.
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Probe #9870 used
                                                                                                           WO200157272-A2
                                                                                                                                                                                                                               30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                              Homo sapiens
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AA154224/C
ID AA1542
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DT 17-OCT
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Gaps

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immune-related disorder; ocular disease; organ transplant rejection; infection; diabetes; pain; sexual dysfunction; Alzheimer's disease; metabolic disorder; haematopoietic cancer; mood disorder; cardiant; parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; cardiovascular disease; brain; neuronal-associated disease; dyskinesia; attention disorder; cognition disorder; psychotic disorder; cytostatic; neurological disorder; virucide; nootropic; cerebroprotective; therapy; neurological disorder; virucide; nootropic; cerebroprotective; therapy; hypotensive; munuosuppressive; antipsorialic; analgesic; hypotrensive; antifungal; dual specificity phosphatase; DSP; MAP kinase phosphatase; MKP; migraine; chromosome 8pl1.1-q11.1; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel phosphatase polypeptide useful for treating cancers, Immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases and metabolic disorders
 phosphatase-related disease;
                                                                                                                                                                                                                                     /*tag= a
/product= "Human SGP060 phosphatase polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Manning G,
phosphatase polypeptide;
                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 29; Fig 1; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                            21-DEC-1999; 99US-0173255.
28-DEC-1999; 99US-0175766.
25-JAN-2000; 2000US-0178078.
31-JAN-2000; 2000US-0179301.
                                                                                                                                                                                                                                                                                                                                  21-DEC-2000; 2000WO-US34736
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plowman GD, Martinez R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-418058/44.
P-PSDB; AAE04839.
                                                                                                                                                                                                                                                                                                                                                                                                                                   (SUGE-) SUGEN INC
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                                                                                                                                                                              sapiens
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RJ;

Hill

Sudarsanam S,

The present invention relates to phosphatase polypeptides, nucleotide sequences encoding them, as well as various products and methods useful for the diagnosis and treatment of various phosphatase-related diseases and conditions. Substance that modulates the activity of phosphatase polypeptide is used to treat immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases and metabolic disorders, including cancers of tissues, cancers of haematopoletic origin, diseases of central and peripheral nervous system, Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, viral infections, infections caused by prions, bacteria and fungi, ocular diseases, diabetes, migraines, pain, sexual dysfunction, mood disorders, attention disorders, neurological disorders, hypotension, hypertension, psychotic disorders, neurological disorders, dyskinesias and organ transplant rejection. The present sequence is a DNA encoding human SCP060 phosphatase (DSP) and MAP and MAPP SCP060 gene maps to chromosomal position

Sequence 636 BP; 123 A; 207 C; 182 G; 124 T; 0 other;

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Gaps

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Score 204.2; DB 22; Length 636; Pred. No. 1.5e-36; 0; Mismatches 168; Indels 6;

17.5%; 64.8%;

Matches 321; Conservative

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Similarity

Query Match Local

Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosls; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; ä 426 486 546 710 gtctggcccaagctctacattggcgatgaggcgacggcgctggaccgctataggctgcag 350 306 470 530 590 650 gtcttcgagttggagcggctcctctacacaggcaagacagcctgtaaccatgccgacgag 192 cccgactactaccgcgacatggacatccagtaccacggcgtggaggccgacgacctgcc cccgaggcctatgaggggctgggcatccgctacctgggtgttgaggcccacgactcgcca accttogacctcagtgtcttcttctaccoggcggcagccttcatcgacagaggggtaagc 367 gcctttgacatgagcatccacttccagacggctgccgacttcatccaccgggcgctgagc gacgaccacagtaagatcctggttcactgcgtcatgggccgcagccggtcagccacctg cagccaggagggaagatcctggtgcattgtgctgtggggcgtgagccgatccgccatg gtcctggcctacctgatgatccacaaggacatgaccctggtggacgccatccagcaagtg gccaagaaccgctgcgtcctcccgaaccggggcttttgaagcagctccgggagctggac 351 aaggogggttcacgcacgtgctgaacgcggccacggccgctggaacgtggacactggg Ren F, War Oian XB, Yang Y, Ma Y, Xue AJ, Chen R, χα c, Human polynucleotide SEQ ID NO 715 BP. AAI58512 standard; cDNA; 1878 Asundi V, Wehrman T, 2000US-05488725. 2000US-0552317. 2000US-0598042. 2000US-0653450. 2000US-0653450. 2000US-0653450. 2000US-0633336. 2000WO-US34263 (first entry) 711 aagcagctggtgcag 725 607 cgcaggctgcggcag 621 (HYSE-) HYSEQ INC Liu C, Vang Z, WO200153312-A1. Wang 25-APR-2000; 09-JUL-2000; 19-JUL-2000; leukaemia; ss 26-DEC-2000; 03-AUG-2000; 14-SEP-2000; 22-OCT-2001 21-JAN-2000; 19-OCT-2000; 29-NOV-2000; 26-JUL-2001 Tang YT, Wang J, AAI58512; 9 253 307 427 291 193 411 471 531 591 651 AAI58512 oy ob οý ු අ g ò g ò

AAI62760 standard; cDNA; 1691

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral nervopathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic thateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification.
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| 1111 || 1111 || 1111 || 1111 || 111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gtctggcccaagctctacattggcgatgaggcgacggctggaccgctataggctgcag 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         742 gictggccaggccictaictcggagaccaggacaiggciaacaaccgccgggagciicgc 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                 to human nucleic acids (AAI57798-AAI61369) and
                                                                                                                                                                                    Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         351 aaggeggggtteaegeaegtgetgaaegeggeeeaeggeegetggaaegtggaeaetggg
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Pred. No. 2e-36;
0; Mismatches 168; Indels 6;
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   Drmanac RT;
                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 715; 10078pp; English
   Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.5%;
64.8%;
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                                                                          WPI; 2001-442253/47.
P-PSDB; AAM39356.
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   Zhou P,
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   o'A'
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1156 cgcaggctgcggcag 1170

RESULT 7 AAI62760/c

711 aagcagctggtgcag

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immunosuppressive, antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant, immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine;
                                                                                                 cytostatic; dermatological; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to novel genes (AAI62752-AAI62961) and proteins (AAMA2347-AAAA415) useful for preventing, treating or ameliaring medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel plasma membrane associated proteins useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancer, immune response and neuronal disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 19; 532pp + Sequence Listing; English
                                                                                                Human; nootropic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruben SM;
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                                                                       Human cDNA SEQ ID NO 19.
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P-PSDB; AAM42355.
                                                                                                                                                                                                                                    WO200155449-A1
                                                                                                                                                                                                             Homo sapiens.
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14-JUL-2000;
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25-SEP-2000;
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13-OCT-2000;
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Homo sapiens

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The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancers and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune thacmolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy, and (f) infectious diseases such as viral, bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1206 GTCTTCGAGTTGGAGCGGCTCCTCTACACAGGCAAGACAGCCTGTAACCATGCCGACGAG 1147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                 gcctttgagctggagcggctcttctggaagggcagtccccagtacacccacgtcaacgag 290
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                                                                                                                                                                                                                                                                                                                                                    Score 203.4; DB 22; Length 1691;
Pred. No. 3e-36;
2; Mismatches 168; Indels 6;
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                                                                                                                                                                                                                                                                                              Sequence 1691 BP; 320 A; 512 C; 480 G; 375 T; 4 other;
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64.4%;
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                                                                                                                                      colitis; (c) cardiovascul (d) wound healing; (e) ne epilepsy; and (f) infections.
                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 64.4
Matches 319; Conservative
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Best Local S
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This invention relates to an isolated dual specificity phosphatase-9 (DSP-9) and its variant. The DSP-9 protein has the ability to dephosphorylate an activated mitogen activated protein (MAP) kinase. Included in the invention are an expression vector comprising a polynucleotide encoding the DSP-9 protein, a host cell transformed by the expression vector, and an antibody that specifically binds to DSP-9. DSP-9 has cytostatic; immunosuppressive; antiallergic; and antiproliferative activity. DSP-9 modulating agents are useful for modulating a proliferative response, differentiation or survival of a cell which displays contexting inhibition of cell growth, anchorage independent growth or an altered intercellular adhesion property, in a patient. DSP-9 agonists and antagonists are also useful for treating a disorder associated with DSP-9 activity such as Duchenne muscular dystrophy, cancer, graft-versus-host disease, autoimmune disease, albormal cell growth, abnormal cell proliferation and cell cycle abnormalities. The present sequence
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                                                                                                                                                                                                                                                                                                     Dual specificity phosphatase-9 which dephosphorylates activated mitogen-activated protein kinase, used to identify agents that inhibit DSP-9 activity and modulate cell proliferation, differentiation, and
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Pred. No. 4.3e-36;
0; Mismatches 169; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          represents human cDNA encoding DSP-9.
                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Fig 1; 66pp; English
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                                                                                                      2000WO-US09321
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                                                                                                                                                                              (CEPT-) CEPTYR INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; cardiovascular disease; brain; neuronal-associated disease; dyskinesia; attention disorder; cognition disorder; psychotic disorder; cytostatic; neurological disorder; virucide; nootropic; cerebroprotective; therapy; neuroprotective; antibacterial; vulnerary; tranquilliser; antiasthmatic; hypotensive; immunosuppressive; antipsoriatic; analgesic; hypotrensive; antifungal; dual specificity phosphatase; DSP; MAP kinase phosphatase; MRP; migraine; chromosome idqq13,3; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to phosphatase polypeptides, nucleotide sequences encoding them, as well as various products and methods useful for the diagnosis and treatment of various phosphatase-related diseases and conditions. Substance that modulates the activity of phosphatase polypeptide is used to treat immune-related diseases and disorders,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H111
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                                                                  gccaagaaccgctgcgtcctcccgaaccggggctttttgaagcagctccgggagctggac
gtcctggcctacctgatgatccacaaggacatgacctggtggacgccatccagcaagtg
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/product= "Human SGP014 phosphatase polypeptide"
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990S-0175766.
2000US-0178078.
2000US-0179301.
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P-PSDB; AAE04838.
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cardiovascular disease, brain or neuronal-associated diseases and metabolic disorders, including cancers of tissues, cancers of haematopoietic origin, diseases of central and peripheral nervous system, Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, viral infections, infections caused by prions, bacteria and fungi, ocular diseases, diabetes, migraines, pain, sexual dysfunction, mood disorders, attention disorders, cognition disorders, hypotension, hypertension, psychotic disorders, neurological disorders, dyskinesias and organ transplant rejection. The present sequence is a DNA encoding human SCPO14 phosphatase polypeptide. This sequence is classified as dual specificity phosphatase (DSP) and MAP kinase phosphatase (MKP). SGP014 gene maps to chromosomal position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phosphatase; gene therapy; enzyme; cancer; pathophysiological hypoxia; cardiac dysfunction; vascular disorder; myopathy; ectodermal dysplasia; congenital muscle disorder; Papillon-Lefevre syndrome; Cowden disease; Moeblus syndrome; Biornstad syndrome; Bannayan Zonana syndrome; schizophrenia; hamartoma; ss.
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Pred. No. 1.1e-35;
0; Mismatches 190;
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The present invention relates to phosphatase proteins and coding. Sequences. The present sequence is one such phosphatase coding sequence. Phosphatases are enzymes that catalyse the dephosphortation of proteins modified by phosphorylation of serine, threonine or tyrosine residues. The phosphatases are useful for treating a variety of diseases: for example cancer e.g. breast, urogenital, prostate, head, neck, lung cancers, synovial sarcomas, renal cell carcinoma, non-small cell lung cancer, hepatocellular carcinoma, pancreatic endocrine tumours, stomach cancer, glioblastoma, colorectal cancer and thyroid cancer, stomach disorders, myopathies, congenital muscle disorders, Papillon-Lefevre syndrome, Cowden disease, ectodermal dysplasia, Moeblus syndrome, blornsted syndrome, Bannayan Zonana syndrome, schizophrenia and
                                                                                                                                                                                                                                                                                                            New protein phosphatase polypeptide for diagnosing and treating phosphatase related disorders such as cancer, schizophrenia, cardiac dysfunction and/or vascular disorders
                                                                                                                                                                                                                            Flanagan P, Lioubin M;
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                  Homo sapiens.
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0
Ouery Match
17.1%; Score 199.4; DB 22; Length 904;
Best Local Similarity 64.3%; Pred. No. 1.9e-35;
Matches 299; Conservative 0; Mismatches 166; Indels 0;
                       Pred. No. 1.9e-35;
0; Mismatches 166; Indels
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open reading frame; ORFX; detection; cytostatic; hepatotropic;
                                       Human ORFX ORF2098 polynucleotide sequence SEQ ID NO:4195
  ctccgggagctggacaagcagctggtgcagcagaggcgacggtcc
                     AAC76543 standard; cDNA; 1200
                                 08-FEB-2001
                           AAC76543;
               RESULT
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antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatcological; immunosuppressive; antidiamatory; antiviral; antibacterial; antifungal; antirheumatic; antithyrold; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive; ss. WO200058473-A2 sapiens. Ношо

31-MAR-2000; 2000WO-US08621. 31-MAR-1999; 02-APR-1999; 05-APR-1999; 05-OCT-2000

99US-0127607. 99US-0127636. 99US-0127728. 2000US-0540763. 30-MAR-2000;

Sequence 904 BP; 183 A; 282 C; 249 G; 190 T; 0 other;

Σ (CURA-) CURAGEN CORP. Shimkets RA,

WPI; 2000-602362/57.

P-PSDB; AAB42334

Novel nucleic acids and peptides derived from open reading frame X, neurodegenerative disorders and cardiovascular disease proliferative cancers, e.g for treating

Claim 5; Page 3391-3392; 5507pp; English.

antiinflammatory; antibacterial; antiviral; antifugal; antirheumatic; antiinflammatory; antibacterial; antiviral; antifugal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroldism, cholesterol ester storage, systemic lupus antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive;

New cardiovascular system associated protein tyrosine phosphatases are used in the diagnosis and treatment of e.g. immune disorders, anti-proliferative disorders, metabolic disorders and cardiovascular

disorders

2000-293136/25 P-PSDB; AAY92177

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erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
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                                                                                                                                                                                                                                                                                                                       670 geggaegaeaececttettegaeeteagtgtetaetttetgeetgttgetegataeate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cardiovascular system associated protein tyrosine phosphatase 4; CSAPTP-4; cytostatic; immunomodulatory; antidiabetic; virucide; hypotensive; cardiant; tyrosine phosphatase modulator; ss.
                                                                                                         17.1%; Score 199.4; DB 21; Length 1200; 64.3%; Pred. No. 2.1e-35;
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                                                                                                                                Indels
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                                                                                                                                166;
                                                                                                                                0; Mismatches
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98US-0164193.
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                                                                                                                                Conservative
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                                                                                                                    Similarity
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                                                                                                                     Local Simi
nes 299;
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                                                                                                         Query Match
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Matches
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This sequence encodes a cardiovascular system associated protein tyrosine phosphatase 4 (CSAPTP). The CSAPTP nucleic acid and protein molecules are used to modulate requiation of cellular processes. CSAPTP nucleic acid and protein molecules and modulators of CSAPTP activity and card and protein molecules and modulators of CSAPTP activity and expression can be used to treat a subject with a disorder characterized by aberrant CSAPTP expression or activity. These disorder can include an immune disorder, an anti-proliferative disorder, a proliferative disorder e.g. renal and lung carcinomas, a metabolic disorder e.g. disorder e.g. thypertension or coronary heart disease or a disorder rising from improper phosphorylation of a phosphorylated protein. Anti-CSAPTP antibodies are used to isolate CSAPTP by standard techniques, to facilitate the purification of a phosphorylation from cells, to detect CSAPTP protein in cell supernatant for evaluating the level of CSAPTP expression and to monitor protein levels in tissue as procedure. CSAPTP nucleic acids, antibodies and protein molecules can be used in screening assays and in predictive medicine e.g. prognostic assays, monitoring clinical trials and pharmacogenetics.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 197.8; DB 21;
Pred. No. 4e-35;
0; Mismatches 167;
                                                                                                                                                             Claim 1; Page 155-156; 156pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tch 17.0%;
al Similarity 64.1%;
298; Conservative
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Matches 298;
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                                                                                                                                                                                                                                                                                              Cardiovascular system associated protein tyrosine phosphatase 4, CSAPTP-4; cytostatic; immunomodulatory; antidiabetic; virucide; hypotensive; cardiant; tyrosine phosphatase modulator; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 153-154; 156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1..663
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/product= CSAPTP-4
                                                                                                                                                                                                                                  Human CSAPTP-4 coding sequence.
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                                    AAA09031 standard; DNA; 928
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98US-0164193.
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P-PSDB; AAY92177.
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30-SEP-1998;
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AAA09031

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Azimzai Y;
                               gccatccagcaagtggccaagaaccgctgcgtcctcccgaaccggggctttttgaagcag 695
                                                                                                                                                                                                          559 gocatecagaeggtgeaggeecaeegeaatatetgeeetaaeteaggetteeteeggeag 618
aagagcaagctgatccagctgggaatcacccacgttgtgaatgccgctgcaggcaagttc 318
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                     aacgtggacactgggcccgactactgcgcgacatggacatccagtaccacggggtggag
                                                                                                                                                                                                                                                                                                                                                                   CDNA sequence encoding a human phosphorylation effector PHSP-11.
                                                                                                                                                                                                                                                                                                                                                                                       Human; phosphorylation effector; PHSP; proliferative disorder;
immune disorder; neuronal disorder; ss.
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Au-Young J, Gorgone GA, Yue
                                                                                                                                                                                                                              696 ctccgggagctggacaagcagctggtgcagcagaggcgacggtcc 740
                                                                                                                                                                                                                                          Location/Qualifiers
28.77
47.4tag — //ttag — //product - "phosphorylation effector"
                                                                                                                                                                                                                                                                                                      AAZ46148 standard; cDNA; 1023 BP.
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98US-0173482.
98US-0106889.
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98US-0113796.
99US-0173482.
99US-0229005.
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P-PSDB; AAY68779.
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Score 197.8; DB 21; Length 928; Pred. No. 4.4e-35; 0; Mismatches 167; Indels 0;

17.0%; 64.1%;

Best Local Similaria, Matches 298; Conservative

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Query Match

Homo sapiens.

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treatment
                                                                                                                     AA246138-246168 encode human phosphorylation effectors (PHSP), designated PHSP1-PHSP31 (the protein sequence for PHSP28 is not given in the specification). The sequences were isolated from cDNA libraries prepared from various human tissues. The PHSP proteins are useful for the diagnosis, treatment and prevention of proliferative disorders, immune disorders and neuronal disorders. The PHSP proteins form pharmaceutical compositions which useful for treating or preventing disorders associated with decreased PHSP expression/activity. PHSP antagonists are useful for treating or preventing disorders associated with increased PHSP expression/activity.
                                          prevention of proliferative, immune and neuronal disorders
                      diagnosis,
                      for the
                    phosphorylation effectors useful
                                                                                   Page 125; 142pp; English
                      human
                                                                                   Claim 9;
                    New
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Sequence 1023 BP; 219 A; 295 C; 299 G; 210 T; 0 other;

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726
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                                                               acccacytcaacyayytctyycccaayctctacattyycgatyaayycgacyycytyyac 335
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0; Mismatches 167; Indels
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Best Local Similarity 64.1%;
Matches 298; Conservative
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Mitogen-activated protein kinase; MAP kinase; dual-specificity phosphatase; DSP-7; cytostatic; immunosuppressive; antiallergic; apoptosis modulation; gene expression modulation; buchenne muscular dystrophy; cancer; graft-versus-host disease; autoimmune diseases; allergy; metabolic disease; ss.
                            BP.
                          AAC62749 standard; cDNA; 1300
                                                                                                                   Human DSP-7 cDNA.
                                                                                    05-FEB-2001
                                                        AAC62749
              AAC62749
RESULT
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The present sequence is given in a method relating to the bosphateae Dep-7. The antibody specific to DSP-7 and the antisense polymucleotide of the nucleic acid encoding DSP-7 and the antisense polymucleotide of the nucleic acid encoding DSP-7 are useful for detecting DSP-7 expression in a sample which comprises an RNA or cDNA preparation. The antibody is linked to a support material and a detectable marker and the amount of DSP-7 polymucleotide hybridisation assay. The isolated DSP-7 polymucleotide is determined using PCR or hybridisation hat modulate DSP-7 activity. The identified agents are useful for treating buchenne muscular distribution, cancer, graft-versus-host disease, autoimmune diseases, allergies, metabolic diseases, abnormal cell growth, abnormal cell proliferation and cell cycle abnormalities.
                                                                                                                                                                                                                                                                                                                            Novel dual-specificity mitogen-activated protein kinase phosphatase polypeptide used in assays to identify agents that modulate the enzyme's activity, which are useful for treating cancer and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1300 BP; 266 A; 398 C; 374 G; 262 T; 0 other;
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                                                                                                        2000WO-US09257
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                                WO200060098-A1
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515 575 455 829 695 aagagcaagctgatccagctgggaatcacccacgttgtgaatgccgctgcaggcaagttc 709 710 caggitgacacaggigccaaaitciaccgiggaaigicciiggagiactaiggcaicgag 769 Gaps ogctctgccacacttgtcctggccttcctcatgatctgtgggaacatgacgctggtagag 590 aaccatatcgatgaggtctggcccagcctcttcctgggagatgcgtacgcagcccgggac cgctataggctgcagaaggcgggttcacgcacgtgctgaacgcggcccacggctgg gccgacgacctgcccaccttcgacctcagtgtcttcttctacccggcggcagccttcatc 516 gacagagcgctaagcgacgaccacagtaagatcctggttcactgcgtcatgggccgcagc cgagetgeecteagtgtteeceaaggeegegtgetggtacaetgtgeeatgggggtaage cggtcagccacctggtcctggcctacctgatgatccacaaggacatgacctggtggac gccatccagcaagtggccaagaaccgctgcgtcctcccgaaccggggcttttgaagcag ; 0 Length 1300; Indels 0; Mismatches 167; Score 197.8; DB 2 Pred. No. 4.9e-35; 17.08; 64.18; 298; Conservative Query Match Best Local Similarity Matches 298; Conserv 920 950 336 456 216 989 qq δ.. qq qa . ò g ò 0y qq ζý qq. ò ò

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_unclassified:\*

sp\_vertebrate:\*

sp\_rodent:\* sp\_plant:\* sp\_virus:\*

sp\_human:\*
sp\_invertebrate:\*
sp\_mammal:\*

sp\_archea:\* sp\_bacteria:\* sp\_fung1:\*

SPTREMBL\_17:\*

Database :

sp\_organelle:\* sp\_phage:\*

sp\_mhc:\*

# SUMMARIES

	Description	O9av17 mus musculu	Oguilé homo sapien	O9da25 mus musculu	Q9bv47 homo sapien	Q9d700 mus musculu	Q9vwn2 drosophila	Q9d7x3 mus musculu	Q9btw0 homo sapien	Q9nrw4 homo sapien	044128 caenorhabdi	Q9zr37 arabidopsis	Q9.lug6 arabidopsis	Q9ffa8 arabidopsis	Q99n11 mus musculu	Q9m8k7 arabidopsis	Q99kc2 mus musculu	Q9nky1 drosophila		Q13524 homo sapien
	ID	090YJ7	91116	09DA25	Q9BV47	002060	Q9VWN2	Q9D7x3	Q9BTW0	Q9NRW4	044128	Q92R37	950760	Q9FFA8	Q99N11	Q9M8K7	Q99KC2	Q9NKY1	Q9NSW1	013524
	DB	17	4	11	4	11	ស	11	4	4	S	10	10	10	11	10	11	S	4	4
	Query Match Length DB	198	198	198	211	198	245	185	98	184	365	198	198	946	184	167	436	1045	303	394
æ	Query Match	39.7	39.7	39.2	38.3	37.9	29.8	28.9	20.1	17.7	17.6	17.5	17.5	17.4	17.2	17.2	16.6	16.6	16.6	16.6
	Score	461	460.5	455	445	440	345.5	335	233	205	204.5	203.5	203.5	201.5	200	199.5	193	193	192.5	192.5
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Q13649 homo saplen Q9aty4 zea mays (m Q9c5s1 arabidopsis Q9vu80 drosophila	. Q91790 xenopus lae Q9by84 homo sapien Q9c0g3 homo sapien Q95147 homo sapien	gall homo mus	099n12 mus musculu 060970 mus musculu 09dcf8 mus musculu	Q9vnv8 drosophila Q9czy9 mus musculu Q99mg6 mus musculu Q9cs15 mus musculu	Q9d715 mus musculu Q9essO mus musculu Q46122 drosophila	mus rosc mus aenc
213649 Q9ATY4 Q9C5S1 29VU80	Q91790 Q9BY84 Q9C0G3 095147	042253 Q9Y6W6 Q9D6P6	099N12 Q60970 Q9DCF8	29VHV8 Q9CZY9 Q99MG6 Q9CSL5	09D715 09ESS0 046122	09JLY7 09JVW4 060969 093592
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### ALIGNMENTS

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Nakamura K., Shima H., Watanabe M., Haneji T., Kikuchi K.; "Molecular cloning and characterization of a novel dual-specificity protein. phosphatase possibly involved in spermatogenesis."; Biochem. J. 344:819-825(1999).
                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                       P SEQUENCE FROM N.A.

Aoyama K., Matsuda T., Aoki N.;
Molecular cloning of a novel dual specificity phosphatase.";
EMBL; AB027003; BAA89411.1;
R EMBL; AF237620; AAK15037.1;
R EMBL; AF237620; AAK15037.1;
R MCD; MGI:1351599; buspp3.
R InterPro; IPR000340; DS.phosphatase.
R InterPro; IPR000340; DS.phosphatase.
R InterPro; IPR00387; TYR_phosphatase.
R PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
R PROSITE; PS0056; TYR_PHOSPHATASE_2; 1.
R PROSITE; PS0056; TYR_PHOSPHATASE_2; 1.
R PROSITE; PS0056; TYR_PHOSPHATASE_1; 1.
                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2001 (TrEMBLrel. 17, Last annotation update)
PROTEIN PHOSPHATASE (DUAL-SPECIFICITY PHOSPHATASE TS-DSP6).
                                        198 AA.
                                          PRT;
                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
MEDLINE-20053896; PubMed-10585869;
                                          PRELIMINARY;
                                      090YJ7
RESULT
                   090YJ7
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Length 198; Score 461; DB 11; Pred. No. 5.4e-36; 39.78; Query Match Best Local Similarity

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PRELIMINARY;
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                                                                                        Mus musculus (Mouse)
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                     PKMEEEGEEEDYCTPGAFELERLFW-KGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAG 80
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"Molecular cloning and characterization of a novel dual-specificity
protein phosphatase possibly involved in spermatogenesis.";
Blochem. J. 344.819-825(1999).
EMBL, AB027004; BAA89412.1;
HSSP; P51452; IVHR.
InterPro; IPR000340; DS_phosphatase.
InterPro; IPR000340; DS_phosphatase.
Fam: PF00782; DSPC; I.
SMART; SM00195; DSPC; I.
                                                                                                            141 SKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQL
                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 SKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQL
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PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
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MEDLINE-20053896; Pubmed-10585869;
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Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L., Staubli F., Sizuki R., Tomita M., Magner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Brownstein M.J., Bult C., Eletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sazaki H., Sato K., Schoenbach C., Schoenbach C., Whittaker C., Willming L.,
Winshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 FTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDH 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 PKMEEEGEEEDYCTPGAFELERLFW-KGSPOYTHVNEVWPKLYIGDEATALDRYRLOKAG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C2492A88D6CC6C2B CRC64;
                                                                                   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DUAL SPECIFICITY PHOSPHATASE 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.2%; Score 455; DB 11
49.2%; Pred. No. 2e-35;
Live 32; Mismatches 6
198 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00195; DSPC; 1.
SMART; SM00012; PTPC_DSPC; 1.
PROSITE; PS00383; TYR_PHOSPHARSE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000340; DS_phosphatase.
InterPro; IPR000387; TYR_phosphatase.
                                                        (TrEMBLrel. 17, Created)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-C57BL/6J; TISSUE-TESTIS;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 409:685-690(2001).
EMBL; AK006247; BAB24480.1; -.
MGD; MGI:1351599; Dusp13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22506 MW;
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Best Local Similarity 49.28
Matches 93; Conservative
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RESULT

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AK009781; BAB26501.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CG7378 PROTEIN.
                                                                                                                                                                                                                                                                                Hydrolase.
                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09VWN2
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  STRAIN-C57BL/65; TISSUE-TONGUE;

KRDLINE-21085660; PubMed-11217851;

KRAIN-C57BL/65; Shibadea A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arawa J., Shibadea A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburrer M., Batalov S., Casavant T.,

Rielschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

Kadota K., Matsudo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomitan M., Magner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Kuyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Winshaw-Boolis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

M. Washi, V. V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ξ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46 FELERLLYTGKTACNHADEVWPGLYLGDQDMANNRRELRRLGITHVLNASHSRWR--GTP 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 FELERLFWKGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                            Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 38.3%; Score 445; DB 4; Length 211; Best Local Similarity 54.3%; Pred. No. 1.9e-34; Matches 89; Conservative 26; Mismatches 47; Indels
                                                                                                                               UNKNOWN (PROTEIN FOR MGC:1136).
Momo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC001613; AAH01613.1; -
SEQUENCE 211 AA; 23945 MW; 60E944304905086D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQLVQ 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 LAYLMLYHHLTLVEAIKKVKDHRGIIPNRGFLRQLLALDRRLRQ 207
                                                                           01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
211, AA
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                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 2310043K02RIK PROTEIN.
                                                    (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                    TISSUE-LUNG CARCINOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2310043K02RIK.
                                                    01-JUN-2001
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09D700
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adamstides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Admanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champen M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Abril J.F., Agbayani A., Burer B.C., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Bernes P.V., Berman B.P., Bhandari D., Boolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Brokstein P., Brottler P.,
RA Borkova D., Botchan M.R., Bouler H., Cadieu E., Center A., Chandra I.,
RA Grerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Durbin K.J., Evorgelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Posler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeqwam C.,
Alalali M., Ralush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             39 FELERLFWKGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FELERLLYTGKTACNHADEVWPGLYLGDQDMANNRRELRRLGITHVLNASHNRWR--GTP 90
                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                       Length 198;
                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                             198 AA; 22419 MW; 11F0CAF4B5620F0E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQLVQ 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                          49;
                                                                                                                                                                                                                                                                                                                                     Ouery Match 37.9%; Score 440; DB 11; Best Local Similarity 54.3%; Pred. No. 5.3e-34; Matches 89; Conservative 24; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 AA
                                                                       pfam; pr00782; DSPc; 1.
SMART; SM00195; DSPc; 1.
SMART; SM0012; PTPC_DSPc; 1.
PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
                                                                                                                                                                                                                                                                                                                                                                                       24; Mismatches
                     InterPro; IPR000340; DS_phosphatase.
InterPro; IPR000387; TYR_phosphatase.
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01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-JUN-2001 (TrEMBLrel. 17, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
MGD; MGI:1914209; 2310043K02R1k.
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NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9BTW0
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RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Palazaclo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazacolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Stradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Walnstock G.M., Welssenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Albeng X.H., Zhong W., Zhong W., Zhus G., Zhao Q., Zheng L.,
RA Jeng X.H., Zhong W., Zhou W., Zhu S., Zhu X., Smith H.O.,
RA Jheng X.H., Myers E.W., Rubin G.M., Venter J.C.;
R. Schence 287:2185-2195 (2000)
B. RHS.P. PS1452: 1U4R.
B. Share Shagnol3976; CG7378
InterPro: IPR000340; DS_phosphatase.
B. RASP: PS1452: DSPC: 1.
B. RRS: PS00105; TR_Phosphatase.
B. RRST: SMOULTS: DSPC: 1.
B. RRST: SMOULTS: PS50054: TYR_PHOSPHATASE_2; 1.
B. RRST: R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 NEVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHG-RW-NVDTGPDYYRDM-DIQYHGVE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 ---KILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDK 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 ADDLPTFDLSVFFYPAAAFIDRALSDDHS-----141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 29.8%; Score 345.5; DB 5; Length 245; Best Local Similarity 45.1%; Pred. No. 6.4e-25; Matches 82; Conservative 21; Mismatches 42; Indels 37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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236 EL 237
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Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchioni L., Mashina J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94 VDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSR 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 LSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELERLFWKGSPQYT----HVNEVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGR--WN 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
                                                                                                                                                                                                                                                                                                                                      "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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EMBL; AK00874; BAB25864.1;

MGD; MGI.191599; 2210015003Rik.

InterPro; IPR000340; DS_phosphatase.

InterPro; IPR000387; TYR_phosphatase.

InterPro; IPR000387; TYR_phosphatase.

SMART; SM0012; DSPC; 1.

SMART; SM00112; PTPC_DSPC; 1.

RPOSITE; PS00383; TYR_PHOSPHATASE_1; UNKNOWN_1.

RPOSITE; PS0056; TYR_PHOSPHATASE_2; 1.

RPOSITE; PS00564; TYR_PHOSPHATASE_2; 1.

REQUENCE 185 AA; 20472 MW; 62E519E41BE575D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria; Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 20.1%; Score 233; DB 4; Length 86 Best Local Similarity 58.5%; Pred. No. 7.6e-15; Matches 48; Conservative 15; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003115.1; -
SEQUENCE 86 AA: 9652 MW; 4DD29AFD5989528B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SATLVLAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQLVQQ
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
UNKNOWN (FROTEIN FOR MGC:2627).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

28.9%; Score 335; DB 11;
Best Local Similarity 43.5%; Pred. No. 4.4e-24;
Matches 74; Conservative 33; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RCVLPNRGFLKQLRELDKQLVQ 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
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SEQUENCE FROM N.A.
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAK-N 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 TKFFPEAISFIDDARRND-SACLVHCLAGISRSVTICLAYLMKTEMCTLDSAYEWVQKRN 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 LYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDL 121
  Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkee Smaldon N., Snith A., Sonnhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudlan M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gupta R., Huang Y., Kieber J., Luan S.;
Identification of a dual-specificity protein phosphatase that
inactivates a MAP kinase from Arabidopsis.";
Plant J. 16:581-589(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; Y18620; CAA77232.1; -.
                                                                                                                                                                                                                       Geisel C., Wamsley P.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                       the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
SEQUENCE 365 AA; 41101 MW; 1E416C0E9693AF66 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.6%; Score 204.5; DB 5
38.6%; Pred. No. 2.5e-11;
tive 24; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ¥.
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                                                                                                                                                                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, Created)
01-WAY-1999 (TrEMBLrel. 10, Last seq
01-UN-2001 (TrEMBLrel. 17, Last and
0SPTPI PROTEIN.
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MEDLINE=99155801; PubMed=10036776;
., Percy C., Rifken L., ., Smith A., Sonnhammer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 RCVLPNRGFLKQLRELDKQL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : || |: || : || 302 ASIAPNFHFMGQLTDYEKML 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00195; DSPc; 1
SMART; SM00450; RHOD; 1
                                                                                                                                Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00782; DSPc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
es 54; Conserv
                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=BRISTOL N2; Geisel C., Wamsley
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                Waterston R.;
Submitted (DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gupta R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                elegans.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 ADDLPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVD 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-9150718; PubMed-7906398; MEDLINE-9150718; PubMed-7906398; Mullson R., Anderson K., Baynes C., Berks M., Wilson R., Anderson K., Baynes C., Berks M., Coulson B., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A., Carton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                         Homo sapiens (Human).
Washaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22;
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Gu J., Huang O., Yu X., Xu S., Wang Y., Han Z., Chen Z., Zhou Y., Gu W., Fu G., Huang C.;
"Novel genes expressed in hematopoletic stem/progenitor cells myelodysplastic Syndromes pattent.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF165519; AAF86649.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 AIQOVAKNR-CVLPNRGFLKQLRELDKQLVQQRRR-----SQRQDGEE 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 184;
           (1) 电影
                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MITOGEN-ACTIVATED PROTEIN KINASE PHOSPHATASE X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20910 MW; B3F962A087C2BA20 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
                                                                                       184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000340; DS_phosphatase.
InterPro; IPR000387; TYR_phosphatase.
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                                                                                       PRT;
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                                                                                                                           (TrEMBLrel. 15, TrEMBLrel. 15, (TrEMBLrel. 17,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 AA;
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                                                                                                                              01-OCT-2000
01-OCT-2000
01-JUN-2001
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Embryophyta; Tracheophyta;
edons; core eudicots; Rosidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAK-NRCVLPNRGF 189
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M., Miyajima N., Tabata S.; "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequenc features of the 1.6 Mb regions covered by twenty physically assigned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -- VWPKLYIGDEATA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 946;
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PROSITE; PS50054; TYR_PHOSPHATASE_LOL; 1.
PROSITE; POS00142; ZINC_PROFFASE; UNKNOWN 1.
SEQUENCE 946 AA; 106195 MW; 39D6967COAC6FED7 CRC64;
                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eeurosids II; Brassicales; Brassicaceae; Arabidopsis: NCBI_TaxID=3702;
                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILARITY TO DSPTP1 PROPEIN.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10;
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es 75;
                                                                                                                                                                             AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.4%; Score 201.5;
32.6%; Pred. No. 1.7e
ive 24; Mismatches
                                                                                                                                                                           946
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EMBL; AB005244; BAB10045.1; -

EMBL; AB025633; BAB10045.1; -

INCEPPO: IPR000340; DS_phosphatase.

INCEPPO: IPR000387; TYR_phosphatase.

INCEPPO: IPR000387; TYR_phosphatase.

INCEPPO: IPR000387; TYR_phosphatase.

INCEPPO: IPR000130; Zn_MTpeptdse.

Pfam; PF00782; DSPC; 1.

SMART; SM00125; DSPC; 1.

SMART; SM00125; PTPC_DSPC; 1.

SMART; SM00355; ZnFC_CH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGEEEDYCTPGAFELERLFWKGSPQYTHVNE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
                                                   176 QVAKNRCVL-PNRGFLKQLRELDKQL 200
                                                                           164 HVKSKRPVASPNAGFIRQLQDLEKSM 189
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97471969; PubMed=9330910;
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                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      853 ARILINLDKK 862
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les 62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clones.
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Q99N11;
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Matches
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09FFA8
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                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                               116 LPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYIGDEATALDRYRLQKAGFTHVLNA-----AHGRWNVDTGPDYYRDMDIQYHGVEADD 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 LPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQ 175
                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                        21;
                                                                                                                                                                         Length 198;
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                                                                                                                                                                                                        51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FAST.
STRAIN-COLUMBIA.
SATO. S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Ta
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EMBL; AB023036; BAB02780.1; -.

EMBL; AB023036; BAB02780.1; -.

InterPro; IPR0000340; DS__phosphatase.

Ffam; PF00782; DSPC; 1.

SNART; SM00195; DSPC; 1.

PROSITE; PS50056; TYR_PHOSPHATASE_DOAL; 1.

PROSITE; PS50054; TYR_PHOSPHATASE_DOAL; 1.

SEQUENCE 198 AA; 22113 MW; 815BBCBE3BFB696A CRC64;
                                                                              PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
SEQUENCE 198 AA; 22017 MW; EBFIC98A177E6450 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
DUAL-SPECIFICITY PROTEIN PHOSPHATASE-LIKE PROTEIN.
                                                                                                                                                                        DB 10;
                                                                                                                                                                    Score 203.5; DB 1
Pred. No. 1.4e-11;
                                                                                                                                                         17.5%; Scc. 37.0%; Pred. No. 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198 AA
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HSSP; Q16828; 1MKP.
InterPro; IPR000340; DS_phosphatase.
InterPro; IPR000387; TYR_phosphatase.
Pfam; PF00782; DSPc; 1.
SMART; SM00195; DSPc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                  176 QVAKNRCVL-PNRGFLKQLRELDKQL 200
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MEDLINE=20277480; PubMed=10819329;
                                                                                                                                                                                                        54; Conservative
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Best Local Similarity
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ses 54; Conserv
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115 DLPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAI 174
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Job time: 193 sec
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                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
AOyama K., Matsuda T., Aoki N.;
Aoyama K., Matsuda T., Aoki N.;
"Molecular cloning of a novel dual specificity phosphatase TS-DSP2.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF237619; AAK15038.1; -.
SEQUENCE 184 AA; 20997 WW; 64953325E88AB577 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 VNEVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRDM--DIQYHGVE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 ADDLPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVD 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 MSOILPGLYIGNEKDARDAEQLSRNKVTHILSV------HDTARPMLEGVKYLCIP 54
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                                                                                                                         Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.2%; Score 199.5; DB 10; Length 167; 36.1%; Pred. No. 2.7e-11; tive 24; Mismatches 61; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 AIQOVAKNR-CVLPNRGFLKQLRELDKQLVQQRRRSQRQDGEEEDGRE 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50056; TYR_PHOSPHATASE_2: 1.
PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
SEQUENCE 167 AA: 18431 MW; 57D722910B79A900 CRC64;
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update) .
DUAL SPECIFICITY PHOSPHATASE TS-DSP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) PUTATIVE DUAL-SPECIFICITY PROTEIN PHOSPHATASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 17.2%; Score 200; DB 11; Best Local Similarity 33.9%; Pred. No. 2.8e-11; Matches 57; Conservative 27; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167 AA
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(TrEMBLrel. 15, I
(TrEMBLrel. 17, I
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                                                                                                        musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F28L1.5.
Arabidopsis thaliana
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STRAIN-CV. COLUMBIA;
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Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                                   NCBI_TaxID=10090;
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COMPUTER READABLE FORM

## GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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; Search time 12.75 Seconds
(without alignments)
388.292 Million cell updates/sec
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1 MTSGEVKTSLKNAYSSAKRL......VQQRRRSQRQDGEEEDGREL 220
                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                 212252 seqs, 22503292 residues
                                 8, 2002, 15:44:11
OM protein - protein search, using sw model
                                                                                                                                                                              OLIGO
Gapop 60.0 , Gapext 60.0
                                                                                                           US-09-847-519A-2
                                 February
                                                                                                                        Perfect score:
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/cgn2\_6/ptodata/2/laa/5A\_COMB.pep:\*
/cgn2\_6/ptodata/2/laa/5B\_COMB.pep:\*
/cgn2\_6/ptodata/2/laa/6A\_COMB.pep:\*
/cgn2\_6/ptodata/2/laa/6B\_COMB.pep:\*
/cgn2\_6/ptodata/2/laa/PcTUS\_COMB.pep:\*
/cgn2\_6/ptodata/2/laa/PcTUS\_COMB.pep:\* Database :

Post-processing: Listing first 1000 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Sequence 4, Appli
Sequence 5, Appli
             Description
                             US-09-013-881-4
US-09-164-193-5
            Π
                              4 4
Query
Match Length DB
                            207
263
          Score
Result
          <u>و</u>
```

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GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                             E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
ALIGNMENTS
                                                                   US-09-013-881-4; Sequence 4, Application US/09013881; Patent No. 6132964
                                                                                                                                                                                                                                                                                                                                                     Palo Alto
                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                     STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                    STREET:
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Search completed: February 8, 2002, 15:46:05 Job time: 114 sec

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GENERAL INFORMATION:
APPLICANT: Acton, Susan L.
TITLE OF INVENTION: NOVEL CSAPTP NUCLEIC ACID MOLECULES AND USES THEREFOR (as amerite Reference: MNI-051
CURRENT APPLICATION NUMBER: US/09/164,193C
CURRENT FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 5
LENGTH: 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 12; DB 4; Lei
Pred. No. 0.00039;
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Pred. No. 0.00048;
0; Mismatches 0;
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEM for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/013,881
                                                                                                                                                      APPLICATE
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 2
US-09-164-193-5
'S Sequence 5, Application U$/09164193C
'Patent No. 6228582
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100.0%; Pre
0;
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LENGTH: 207 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 SRSATLVLAYLM 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153 SRSATLVLAYLM 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
US-09-164-193-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 SRSATLVLAYLM 163
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Best Local Similarity
Matches 12; Conserva
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Best Local Similarity
Matches 12; Conserv
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                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-013-881-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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OM protein - protein search, using sw model

February 8, 2002, 15:42:06 ; Search time 11.67 Seconds
(without alignments)
691.196 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-847-519A-2 1161 1 WTSGEVKTSLKNAYSSAKRL......VQQRRRSQRQDGEEDGREL 220

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 segs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SITMMARTES

		Description	рошо	уошо	homo	rattu	Q05922 mus musculu		Q9pw71 gallus gall			Q63340 rattus norv	Q16829 homo sapien	-	Q64623 rattus norv	homo	O09112 mus musculu		rattu	Q16690 homo sapien	Q39491 chlamydomon	Q10038 caenorhabdi	P40479 saccharomyc	Q9uni6 homo sapien	P38590 saccharomyc			P34680 caenorhabdi		•	4	O10273 orgyia pseu	Q05909 mus musculu	_	Q00684 saccharomyc
SUMMARIES		di	DUS3_HUMAN	DUS9_HUMAN	DUS4_HUMAN	DUS4_RAT	DUS2_MOUSE	DUS2_HUMAN	DUS4_CHICK	DUS1_HUMAN	DUS5_RAT	DUS7_RAT	DUS7_HUMAN	DUS1_MOUSE	DUS1_RAT	DUS8_HUMAN	· DUS8_MOUSE	DUS6_HUMAN	DUS6_RAT	DUS5_HUMAN	PTP3_CHLEU	VHP1_CAEEL	YIL3_YEAST	DUSC_HUMAN	MSG5_YEAST	PVH1_YEAST	VH01_VACCV	YO42_CAEEL	VH01_RACVI	VH01_VACCC	VH01_VARV	PTP2_NPVOP	PTPG_MOUSE	PTPG_HUMAN	CC14_YEAST
		Length DB	185 1	384 1	394 1		•		375 1																							160	42	1445 1	21
đ	Query	Match	29.8	٠	16.	16.	15.	15.	7	14.	14.	14.	74	14	-	14	14	13	73	_	1	7	7	11.	10	01	σ		σ	9.5	9.1	8.4	8.4		7.8
		Score		196.5	192.5	192.5	184.5	180.5	180	169	168.5	166	166	166	166	163	163	161.5	161.5	157.5	136.5	132.5	132	128.5	124.5	122	113	111	108	107	106	σ	97.5	93.5	91
	Result	NO.	1	7	٣	4	S	9	7	ω.	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	en en

llus gall	ccharomyc	mo sapien	rattus norv	s musculu	cherichia	mo sapten	mo sapien	ndida alb	osophila	ttus norv	ttus norv	
Q98936 ga	P38148 sa	P22105 ho	Q62656 ra	P48441 mu	P76093 es	P54252 ho	P23471 ho	P43078 ca	Q9w1k5 dr	P70569 ra	P20417 ra	
PG_CHICK	9T_YEAST	NX_HUMAN	PTP2_RAT	JA_MOUSE	3D_ECOLI	O1_HUMAN	PZ_HUMAN	PX_CANAL	ST_DROME	5B_RAT	N1_RAT	
1 PTI	1 YB	1 TEI	1 PTI	1 ID	1 YNJ	1 MJI	1 PTI	1 PT	1 SE	1 MY!	1 PTI	
1422	807	4289	2316	634	430	360	2314	597	497	1846	432	
7.8	7.2	7.2	7.2	6.9	6.9	8.9	6.8	8.9	6.7	6.7	9.9	
91	84	84	83.5	80.5	80	79.5	79.5	78.5	78	78	77	
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                                                                                                                           88 AHGR--WNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILV 145
                                                                                                                                             63 AEGRSFMHVNTNANFYKDSGITYLGIKANDTQEFNLSAYFERAADFIDQALAQKNGRVLV 122
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37 GAFE-----LERLFWKGSPQYT----HVNEVWPKLYIGDEATALDRYRLQKAGFTHVLNA 87
                                                                                           3 GSFELSVQDLNDLLSDGSGCYSLPSQPCNEVTPRIYVGNASVAQDIPKLQKLGITHVLNA 62
                                                                                                                                                                                                           146 HCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQLVQQ 203
                                                                                                                                                                                                                                                                                                                                              15-DEC-1998 (Rel. 37, Last Sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DUAL SPECIFICITY PROTEIN PHOSPHATASE 9 (EC 3.1.3.48) (EC 3.1.3.16)
(MITOGEN-ACTIVATED PROTEIN KINASE PHOSPHATASE 4) (MAP KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN TYROSINE + PHOSPHATE.
-!- SUBGELULAR LOCATION: CYTOPLASMIC.
-!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                  11;
 29.8%; Score 346.5; DB 1; Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN-TYROSINE PHOSPHATASE.
                                Indels
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F8598CA95AB379B7 CRC64;
                                54;
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PROSITE; PSS0056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
                Pred. No. 8.2e-27
                                                                                                                                                                                                                                                                                                    384 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000340; DS_phosphatase.
InterPro; IPR001763; Rhodanese_domain.
InterPro; IPR000187; TYR_phosphatase.
Pfam; PF007082; DSPc; 1.
SMART; SM00195; DSPc; 1.
                                                                                                                                                                                                                                                                                                    PRT;
                              35;
                                                                                                                                                                                                                                                                                                                                15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last seq
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                43.88;
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                              78; Conservative
                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                              PHOSPHATASE 4) (MKP-4)
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290
384 AA;
                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                  DUS9_HUMAN
Q99956;
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SEQUENCE
Query Match
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                                                                                                                                            70 ALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYY-RDMDIQYHGVEADDLPTFDLSVFFYPA 128
                                                                                                                                                                                                                                     273 IEFIDEALS-QNCGVLVHCLAGVSRSVTVTVAYLMQKLHLSLNDAYDLVKRKKSNISPNF 331
                                                                                                         173 DAESEADRDSMSCGLDSEG----ATPPPVGLRASF-----PVQILPNLYLGSARD 218
                                                                                                                                                                                                                  129 AAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRC-VLPNR 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-95221370; PubMed-7535768; Guan K.-L., Butch E.; Issued K.-L., Butch E.; Issued Characterization of a novel dual specific phosphatase, HVH2, which selectively dephosphorylates the mitogen-activated
                                      Gaps
                                                                        12 NAYSSAKR--I.SPKMEEEGEEEDYCTPGAFELERLFWKGSPQYTHVNEVWPKLYIGDEAT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
02-NGG-2001 (Rel. 40, Last annotation update)
DUAL SPECIFICITY PROTEIN PHOSPHATASE 4 (EC 3.1.3.48) (EC 3.1.3.16)
                                                                                                                                                                  -!- SUBCELLULAR LOCATION: NUCLEAR.
-!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHATASE FAMILY: DUAL SPECIFICITY SUBFAMILY.
                                      25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEPHOSPHORYLATING BOTH THR AND TYR RESIDUES ON MAP KINASES ERKI AND ERK2.
Length 384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)0 = PROTEIN TYROSINE + ORTHOPHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein kinase.";
J. Biol. Chem. 270:7197-7203(1995).
-!- FUNCTION: REGULATES MITOGENIC SIGNAL TRANSDUCTION BY
   DB 1;
 16.9%; Score 196.5; DB : 30.5%; Pred. No. 9.7e-12
                                    34; Mismatches.
                                                                                                                                                                                                                                                                                                                                                                                                                  394 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00383; TYR_PHOSPHATASE_1; 1. PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000340; DS_phosphatase.
InterPro; IPR001763; Rhodanese_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000387; TYR_phosphatase.
Pfam; PF00782; DSPC; 1.
Pfam; PF00781; Rhodanese; 1.
SMART; SM00195; DSPC; 1.
SMART; SM00450; RHOD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                       188 GFLKQLRELDKQLVQQRRRSQRQ 210
                                                                                                                                                                                                                                                                                                               EMBL; U21108; AAA85119.1; -.
                                    62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P51452; 1VHR.
                  Best Local Similarity
Matches 62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DUSP4 OR VH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               602747;
                                                                                                                                                                                                                                                                                                                                                                                                                  DUS4_HUMAN
   Query Match
                                                                                                                                                                                                                                                                                                                                                                               DUS4_HUMAN
                                                                                                                                                                               219
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                                                                                                                                               4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDL 116
                                                                                                                                                                                                                          117 PTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQ 176
                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DUAL SPECIFICITY RROTEIN PHOSPHATASE 4 (EC 3.1.3.48) (EC 3.1.3.16)
(MITOGEN-ACTIVATED PROTEIN KINASE PHOSPHATASE-2) (MAP KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Pheochromocytoma;
MEDLINE=95301550; PubMed=7782322;
Misra-Press A., Rim C.S., Yao H., Roberson M.S., Stork P.J.S.;
"A novel mitogen-activated protein kinase phosphatase. Structure,
                                                                                                                                             6
                                                                                                                     DB 1; Length 394;
                        CH2 A DOMAIN.
CH2 B DOMAIN.
PROTEIN-TYROSINE PHOSPHATASE.
                                                                                                                                             58; Indels
                                                                BY SIMILARITY.
0603971759B6952E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression, and regulation.";
J. Biol. Chem. 270:14587-14596(1995).
-!- FUNCTION: REGULATES MITOGENIC SIGNAL TRANSDUCTION
                                                                                                                   Score 192.5; DB 1 Pred. No. 2.5e-11;
                                                                                                                                                                                                                                                                                                                                                                        395 AA
                                                                                                                                             29; Mismatches
PS50054; TYR_PHOSPHATASE_DUAL; 1.
                                                                                                                                                                                                                                                                                             1 : | : | | | : || 335
310 VKQRRSIISPNFSFMGQLLQFESQVL 335
                                                                                                                                                                                                                                                                            177 VAKNRCVL-PNRGFLKQLRELDKQLV 201
                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                            42953 MW;
                                                                                                                   16.6%;
34.2%;
            Hydrolase; Nuclear protein.
                                                                                                                                             50; Conservative
                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
                                      153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHATASE-2) (MKP-2)
                         46
138
197
280
394 AA;
                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DUSP4 OR MKP2
                                                                ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                      DUS4_RAT
                                      DOMAIN
DOMAIN
                           DOMAIN
                                                                                                                                             Matches
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117 PTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQ 176
                                                                                                                                                                                                                                                                                                                                                                                              57 EVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDL 116
                                                                                                                                                                                                                                                                                                                                         Gerondakis S., Economou C., Grumont R.J.;
"Structure of the gene encoding the murine dual specificity tyrosine-
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN TYROSINE + ORTHOPHOSPHATE.
-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- TISSUE SPECIFICITY: IN HEMATOPOIETIC TISSUES SUCH AS SPLEEN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
DUAL SPECIFICITY PROTEIN PHOSPHATASE 2 (EC 3.1.3.48) (EC 3.1.3.16)
DUSP2 OR PACI OR PAC-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=93206122; Pubmed=7681221;
Machan P., Davis P., Moskaluk C.A., Kearns M., Krutzsch H.,
Siebenlist U., Kelly K.;
"PAC-1: a_mitogen-induced nuclear protein tyrosine phosphatase.";
                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: REGULATES MITOGENIC SIGNAL TRANSDUCTION BY DEPHOSPHORYLATING BOTH THR AND TYR RESIDUES ON MAP KINASES
                                                                                                                                                                                                                                                                    Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)0 -
                                                                                                                                                                                               PROTEIN-TYROSINE PHOSPHATASE.
                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                           SIMILARITY. A90EFFD378A050FD CRC64;
                                                                                                                                                                                                                                                                                              58;
                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                  16.6%; Score 192.5; DB 1
34.2%; Pred. No. 2.5e-11;
iive 29; Mismatches 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     318 AA
                                                                                                          PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
Hydrolase; Nuclear protein.
                                                                                                                                                                    CH2 A DOMAIN
CH2 B DOMAIN
          Interpro; IPR000340; DS_phosphatase.
Interpro; IPR001763; Rhodanese_domain.
Interpro; IPR000387; TYR_phosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                     177 VAKNRCVL-PNRGFLKQLRELDKQLV 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=129;
MEDLINE=95203877; PubMed=7896276;
                                                                                                                                                                                                                        43187 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     threonine phosphatase PAC1.";
Genomics 24:182-184(1994).
                                                    Pfam; PF00782; DSPc; 1.
Pfam; PF00581; Rhodanese; 1.
SMART; SM00195; DSPc; 1.
SMART; SM00450; RHOD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 259:1763-1766(1993).
                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                               154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Wonse)
                                                                                                                                                                                                           281
395 AA;
                                                                                                                                                                                                                                                                                 Local Similarity
les 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  060640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DUS2_MOUSE
Q05922; Q6(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THYMUS
                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 50
                                                                                                                                                                                                           ACT_SITE
SEQUENCE
                                                                                                                                                                                 DOMAIN
                                                                                                                                                                    DOMAIN
                                                                                                                                                                                               DOMAIN
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DUS2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 8.. qq
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                         ERK1 AND ERK2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
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                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 FQEAISFID-SVKNSGGRVLVHCQAGISRSATICLAXLIQSHRVRLDEAFDFVKQRRGVI 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 GDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVF 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 FYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 LKNAYSSAKRLSPKMEEEGEEEDYCTPGAFELER-----LFWKGSPQYTHVNEVWPKLYI 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FCB-1994 (Rel. 40, Last annotation update)
DUAL SPECIFICITY PROTEIN PHOSPHATASE 2 (EC 3.1.3.48) (EC 3.1.3.16)
DUAL SPECIFICITY PROTEIN PHOSPHATASE PAC-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 GSCNHSSDLQGLQACGITAVLNVS-----ASCPNHFEGL-FHYKSIPVEDNQMVEISAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                    SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHATASE FAMILY: DUAL SPECIFICITY SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS00383; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2: 1.
PROSITE; PS50056; TYR_PHOSPHATASE_0LA: 1.
Hydrolase; Nuclear protein; Alternative splicing.
ACT_SITE 261 261 BY SIMILARITY.
ACT_SITE 175 179 GGPVE -> VSDL (IN SHORT ISOFORM).
VARSPLIC 175 179 GGPVE -> VSDL (IN SHORT ISOFORM).
VARSPLIC 180 318 MISSTNG (IN REF. 2).
CONFLICT 20 20 A -> V (IN REF. 2).
CONFLICT 156 156 P -> A (IN REF. 2).
SEQUENCE 318 AA; 34546 MW; A2006ED0FD27E41D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.9%; Score 184.5; DB 1; Length 318; 28.3%; Pred. No. 1.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        314 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:101911; Dusp2.
InterPro; IPR000340; DS_phosphatase.
InterPro; IPR001763; Rhodanese_domain.
InterPro; IPR000387; TYR_phosphatase.
Pfam; PF00782; DSPC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00581; Rhodanese; 1.
SMART; SM00195; DSPC; 1.
SMART; SM00450; RHOD; 1.
                                                                                                                                                                                                                                                                                                 EMBL; L11330; AAA19666.1; -. EMBL; U09268; AAA85136.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               299 SPNFSFMGQLLQLETQVL 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 -PNRGFLKQLRELDKQLV 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                  P51452; 1VHR.
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SEQUENCE FROM N.A.
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DUS2_HUMAN
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                                                                                                                                                                                                                                  EVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 PTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'PAC-1: a mitogen-induced nuclear protein tyrosine phosphatase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- TISSUE SFLUCTION: BY MITOGENS.
-1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- CATALYTIC ACTIVITY: PROTEIN TYROSINE.PHOSPHATE + H(2)O PROTEIN TYROSINE + ORTHOPHOSPHATE.
MEDLINE-93206122; PubMed-7681221;
Rohan P., Davis P., Moskaluk C.A., Kearns M., Krutzsch H.,
Siebenlist U., Kelly K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FDD3543C6DE10CA5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: NUCLEAR.
-!- TISSUE SPECIFICITY: IN HEMATOPOIETIC TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.5%; Score 180.5; DB 1
32.2%; Pred. No. 2.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DUS4_CHICK STANDARD; PRT; 375 AA. 09PW71; 20-AUG-2001 (Rel. 40, Created) 20-AUG-2001 (Rel. 40, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00383; TYR_PHOSPHATASE 1; 1. PROSITE; PS50056; TYR_PHOSPHATASE_2; 1. PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000340; DS_phosphatase.
InterPro; IPR001763; Rhodanese_domain.
InterPro; IPR000387; TYR_phosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 : | |: | |: || |: || 287 VKQRRGVISPNFSFMGQLLQFETQVL 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 VAKNRCVL-PNRGFLKQLRELDKQLV 201
                                                                                                                                                                                                             MEDLINE=96070437; PubMed=7590752;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34399 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L11329; AAA50779.1; -. EBMBL; U13853; AAA6112.1; -. HSSP; P51452; IVHR. MIM; 603068; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00782; DSPc; 1.
Pfam; PF00581; Rhodanese; 1.
                                                                                                                      Science 259:1763-1766(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase; Nuclear protein.
ACT_SITE 257 257
SEQUENCE 314 AA; 34399 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 32.29
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00195; DSPc; 1
SMART; SM00450; RHOD; 1
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4

314 QVL 316

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NCBI_TaxID=9606;
                                                                  DUS1_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loca
Matches
                                        RESULT 8
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                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 GFTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDD 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202 GITALLNVS-----SDCPNHF-EGHYQYKCIPVEDNHKADISSWFMEAIEYID-SVKEC 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254 CGRVLVHCQAGISRSATICLAYLAMKKRVKLEKAFEFVKQRRSIISPNFSFMGQLLQFES 313
                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 ISPPSSAESLDLGFSSCGT----PLHDQGGPV-----EILPFLYLGSAYHAARRDMLDAL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 HSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVL-PNRGFLKQLRELDK 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 LSPKMEEEGEEEDYCTPGAFELERLFWKGSPQYTHVNEVWPKLYIGDEATALDRYRLQKA 79
                                                                                                                                                                              Fu S.-L., Waha A., Vogt P.K.; "Identification and characterization of genes upregulated in cells
20-AUG-2001 (Rel. 40, Last annotation update)
DUAL SPECIFICITY PROTEIN PHOSPHATASE 4 (EC 3.1.3.48) (EC 3.1.3.16)
(MITOGEN-ACTIVATED PROTEIN KINASE PHOSPHATASE-2) (MAP KINASE
                                                                                                                                                                                                                               --- FUNCTION: REGULARES MITOGENIC SIGNAL TRANSDUCTION BY DEPHOSPHORYLATING BOTH THR AND TYR RESIDUES ON MAP KINASES ERK1 AND ERK2 (BY SIMILARITY).
--- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)0 --
PROTEIN TYROSINE + ORTHOPHOSPHATE.
--- SUBCELDULAR LOCATION: WOLCLEAR (BY SIMILARITY).
--- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHATASE FAMILY: DUAL SPECIFICITY SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.5%; Score 180; DB 1; Length 375; 30.1%; Pred. No. 3.9e-10; tive 35; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN-TYROSINE PHOSPHATASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
179290D0C2BEEEF1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00303; TYR_PHOSPHATASE_1; 1. PROSITE; PS50056; TYR_PHOSPHATASE_2; 1. PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1. Hydrolase; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CH2 A DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000340; DS_phosphatase.
InterPro; IPR0001763; Rhodanese_domain.
InterPro; IPR000183; TYR_phosphatase.
Pfam; PF00781; DSPc; 1.
Pfam; PF00581; Rhodanese: 1.
SMART; SM00195; DSPc; 1.
                                                                                                                                                       STRAIN-White leghorn;
MEDLINE-20379359; PubMed-10918612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF167296; AAD46656.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41052 MW;
                                                                                                                                                                                                         transformed by v-Jun.";
Oncogene 19:3537-3545(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similaricy
nes 55; Conservative
                                                               Gallus gallus (Chicken).
                                       PHOSPHATASE-2) (MKP-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122
178
361
375 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q16828; 1MKP
                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                 NCBI_TaxID=9031;
                                                   DUSP4 OR MKP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QLV 201
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SEQUENCE
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                                                                                                     Gallus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                            44 LFWKGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRD 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 MDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLM 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216 GHYQYKSIPVEDNHKADISSWFNEAIDFID-SIKNAGGRVFVHCQAGISRSATICLAYLM 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Gaps
                                              01-DEC-1992 (Rel. 24, Created)
01-FBB-1996 (Rel. 33, Last sequence update)
01-FBB-1996 (Rel. 40, Last sequence update)
DUAL SPECIFICITY PROTEIN PHOSPHARASE 1 (EC 3.1.3.48) (EC 3.1.3.16)
(MAP KINASE PHOSPHARASE.) (MKP-1) (PROTEIN-TYROSINE PHOSPHARASE
CLIOO) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH1).
                                                                                                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.6%; Score 169; DB 1; Length 367; 30.2%; Pred. No. 4.5e-09; ive 33; Mismatches 64; Indels
                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN-TYROSINE PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258 BY SIMILARITY.
39297 MW; 11BD1D39A9FCD51F CRC64;
  367 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP, P51452; 1VHR.
MIM; 600714; -
InterPro; 1PR000340; DS_phosphatase.
InterPro; 1PR001763; Rhodanese_domain.
InterPro; 1PR001763; TYR_phosphatase.
Pfam; PF00782; DSPC; 1.
SMART; SM00195; DSPC; 1.
SMART; SM00195; DSPC; 1.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X68277; CAA48338.1; -. PIR; S29090; S29090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 30.2% les 48; Conservative
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase; Cell cycle.
DOMAIN 175 367
                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367 AA;
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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EVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDL 116
                                        |: | ||: | | : | : | : | : | ELLPFLYLGSAYHASKCEFLANLHITALLNVSRRTSEACT-----THLHYKWIPVEDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCB1_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER
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   57
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                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hevroni D., Rattner A., Bundman M., Lederfein D., Gabarah A., Mangelus M., Silverman M.A., Kedar H., Naor C., Kornuc M., Hanoch T., Seger K., Theill L.E., Nedivi E., Richter-Levin G., Citri Y., "Hippocampal plasticity involves extensive gene induction and multiple cellular mechanisms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. MOI. Neurosci. 10:75-98(1998).
-!- FUNCTION: THIS PROTEIN SHOWS BOTH ACTIVITY TOWARD TYROSINE-PROTEIN PHOSPHATE AS WELL AS WITH SERINE/THREONINE-PROTEIN PHOSPHATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CH2 A DOMAIN.
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN TYROSINE + ORTHOPHOSPHATE.
SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY)
SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHAPAEE FAMILY: DUAL SPECIFICITY SUBFAMILY.
SIMILARITY: CONTAINS THE CDC25 HOMOLOGY DOMAINS 2 A AND B (CH2
                                                                                                                                                                                                                                                                                                            15-JUL-1999 (Rel. 38, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.5%; Score 168.5; DB 1; Length 384; 31.5%; Pred. No. 5.3e-09; ive 25; Mismatches 66; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)0 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN-TYROSINE PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
5644069BBD348700 CRC64;
                                  164 IHKDMTLVDAIQQVAKNRCVL-PNRGFLKQLRELDKQLV 201
                                                                                                                                                                                                                                 384 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00383; TYR_PHOSPHATASE_1; 1. PROSITE; PS50056; TYR_PHOSPHATASE_2; 1. PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1. Hydrolase; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CH2 B DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000340; DS_phosphatase.
InterPro; IPR0001763; Rhodanese_domain.
InterPro; IPR000187; TYR_phosphatase.
Pfam; PF00361; DSPc; 1.
Pfam; PF00361; Rhodanese; 1.
SMART; SM00195; DSPc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLY-GLY
                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-98364306; PubMed-9699150;
                                                                                                                                                                                                                                                                                           38, Created)
38, Last seq
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                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rat).
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384 AA;
                                                                                                                                                                                                                                                            )54838;
15-JUL-1999 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACT_SITE
SEQUENCE
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                                                                                                                                                                                               DUS5_RAT
                                                                                                                                                            RESULT
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between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQ 176
                                     Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
DUAL SPECIFICITY PROTEIN PHOSPHATASE 7 (EC 3.1.3.48) (EC 3.1.3.16)
DUSP7 OR MKPX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -:- SUBCELLULAR LOCATION: CYTOPLASMIC.
-:- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-SPRAGUE-DAWLEY; TISSUE-Neuron; MEDLINE=96240(12; PubMed=8626780; Mada M., Boschert U., Dickinson R., Martinou J.C., Martinou I., Camps M., Schlegel W., Arkinstall S.; "MKP-3, a novel cytosolic protein-tyrosine phosphatase that exemplifies a new class of mitogen-activated protein kinase phosphatase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biol. Chem. 271:4319-4326(1996).
-1- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)0
PROTEIN TYROSINE + PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 280;
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45D6F4A92F2BBDDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.3%; Score 166; DB 1; ilarity 31.2%; Pred. No. 6.2e-09; Conservative 29; Mismatches 65
                                                                                                                                                                                                                                                                                                                                    280 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000340; DS_phosphatase.
InterPro; IPR000387; TYR_phosphatase.
                                                                                                                                                    293 IKQRRSVVSPNFGFMGQLLQYESEIL 318
                                                                                                                    177 VAKNRCVL-PNRGFLKQLRELDKQLV 201
                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ΒX
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30668 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X94186; CAA63896.1; -. HSSP; P51452; 1VHR.
                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
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280 AA;
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Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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9

3;

Gaps

6

Conservative

Best Local Similarity Matches 46; Conser

Query Match

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DGESDRELPSSATESD-----GSPVPSSQPAFPVQILPYLYLGCAKDSTNLD--VLGKYG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                          280 QLLDFERTL 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                 FTHVLNAA - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHARACTERIZATION.
                                                                                                                                                                                                                                QLRELDKQL
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                                                                                                                                                                                                                                                                                                                                                                                         DUS1_MOUSE
P28563;
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                                                                                                                                                                                                                                                                                                                                            RESULT 12
DUSI_MOUSE
                                                 81
                                                                                                                                        133
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                                                                                  do oy
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ف
                                                                                                                                 81 FTHVLNAA-----HGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFI 132
DGESDRELPSSATESD-----GSPVPSSQPAFPVQILPYLYLGCAKDSTNLD--VLGKYG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                   OL-NUV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DUAL SPECIFICITY PROTEIN PHOSPHATASE 7 (EC 3.1.3.48) (EC 3.1.3.16)
DUSP7 OR PYST2.
                                                                                132 IKYILNVTPNLPNAFEHG-----GEFTYKQIPISDHWSQ-----NLSQFFPEAISFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
-1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Groom L.A., Sneddon A.A., Alessi D.R., Dowd S., Keyse S.M.; "Differential regulation of the MAP, SAP and RK/p38 kinases by a novel cytosolic dual-specificity phosphatase."; EMBO J. 15:3621-3632(1996).

-!- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)0 - PROTEIN TYROSINE + PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y SIMILARITY.
E89B1C2ABB2E75DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00195; DSPC; 1.
PROSITE; PS00383; TYR_PHOSPHATASE_1; FALSE_NEG.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
                                                                                                                                                                                                                                                                                                                                                                                      322 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000340; DS_phosphatase.
InterPro; IPR000347; TYR_phosphatase.
Pfam: PF00782; DSPc; 1.
SMART; SM00195; DSPc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-96312959; PubMed-8670865;
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                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 35, (Rel. 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234 2
322 AA;
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238 QLLDFERTL 246
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                                                                                                                                                                                                                             192 QLRELDKQL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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01-NOV-1997
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Q16829;
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SEQUENCE
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EGEEEDYCTPGAFELERLFWKGSP----QYTHVNEVWPKLYIG--DEATALDRYRLQKAG 80

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---HGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFI 132
                                                                                                                                DRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRC-VLPNRGFLK 191
                                                                                                                                                                         221 DEARS-KKCGVLVHCLAGISRSVTVTVAYLAQKANLSLNDAYDFVKRKKSNISPNFNFMG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Charles C.H., Abler A.S., Lau L.F.; "CDNA sequence of a growth factor-inducible immediate early gene and characterization of its encoded protein."; Oncogene 7:187-190(1992).
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--- FUNCTION: DUAL SPECIFICITY PHOSPHATASE THAT DEPHOSPHORYLATES MAP
KINASE ERK2 ON BOTH THR-183 AND TYR-185.
--- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O =
PROTEIN TYROSINE + ORTHOPHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                kinase in vivo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
20-AGG-2001 (Rel. 40, Last annotation update)
DUAL SPECIFICITY PROTEIN PHOSPHATASE 1 (EC 3.1.3.48) (EC 3.1.3.16)
MAP KINASE PHOSPHATASE-1) (MAP-1) 
                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-94037096; PubMed-8221888;
Sun H., Charles C.H., Lau L.F., Tonks N.K.;
"MKP-1 (3CH134), an immediate early gene product, is a dual
specificity phosphatase that dephosphorylates MAP kinase in
Cell 75:487-493(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-93360956; PubMed-8355678;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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IPR000340;

us-09-847-519a-2.rsp

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Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DUS8_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 LFWKGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRD 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 LYDQGGPV-----EILSFLYLGSAYHASRKDMLDALGITALINVS-----ANCPNHF-E 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 MDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLM 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annoctation update)
DUAL SPECIFICITY PROPERT PROPERTATES I (EC 3.1.3.48) (EC 3.1.3.16)
(MAP KINASE PHOSPHATASE-1) (MKP-1) (PROFEIN-TYROSINE PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
                                                                                                                                                                                                                                                                                                                                                                                                   14.3%; Score 166; DB 1; Length 367; 30.2%; Pred. No. 8.8e-09; ive 32; Mismatches 65; Indels
                                                                                                                                                                                                                                                                          PROTEIN-TYROSINE PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                     50B5F90FEBBD19AB CRC64;
                                                                                                                                                                                                                                                                                                                    C->S: LOSS OF ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164 IHKDMTLVDAIQQVAKNRCVL-PNRGFLKQLRELDKQLV 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RTNRVKLDEAFEFVKQRRSIISPNFSFMGQLLQFESQVL 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      367 AA
                                                                                                                                    SMARY, SM00195, DSPC, I.
SMARY, SM00195, DSPC, I.
SMARY: SM00450, RHOD; I.
PROSITE; PS00039; TYR_PHOSPHATASE_1; I.
PROSITE; PS50056, TYR_PHOSPHATASE_2; I.
PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; I.
           MGD; MGI:105120; Ptpn16.
InterPro; IPR000140; DS_phosphatase.
InterPro; IPR0001763; Rhodanese_domain.
InterPro; IPR000187; TR_phosphatase.
Pfam; PF00782; DSPc; 1.
Pfam; PF00581; Rhodanese; 1.
                                                                                                                                                                                                                                                                                                                                     MW.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X84004; CAA58828.1; -. HSSP; P51452; 1VHR.
                                                                                                                                                                                                                                                                                                                                     39369
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 30.29
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                  Hydrolase; Cell cycle.
DOMAIN 175 367
                                                                                                                                                                                                                                                                                                               258
367 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DUSP1 OR CL100.
                                                                                                                                                                                                                                                                                         ACT_SITE
MUTAGEN
                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DUS1_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CL100)
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                                                                                                                                                                                                                                                                                                                                                                                                          ς,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inactivates mitogen-activated protein kinase.";
J. Neurochem. 65:1823-1833(1995)
-!- FUNCTION: THIS PROTEIN SHOWS BOTH ACTIVITY TOWARD TYROSINE-PROTEIN
PHOSPHATE AS WELL AS WITH SERINE/THREONINE-PROTEIN PHOSPHATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN TYROSINE + ORTHOPHOSPHATE.
--- TISSUE SPECIFICITY: ABUNDANT IN BRAIN, HEART, AND SKELETAL MUSCLE.
---- SIMILARITY: BELONGS TO THE UNON-RECEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 LFWKGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRD 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 MDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLM 163
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     013202;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DUAL SPECIFICITY PROTEIN PHOSPHATASE 8 (EC.3.1.3.48) (EC.3.1.3.16)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Martell K.J., Seasholtz A.F., Kwak S.P., Clemens K.K., Dixon J.E., "hVH-5: a protein tyrosine phosphatase abundant in brain that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      216 GHYQYKSIPVEDNHKADISSWFNEAIDFID-SIKDAGGRVFVHCQAGISRSATICLAYLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)0 =
                                                                                                                                                                                                                                                                                                                                                            14.3%; Score 166; DB 1; Length 367; 30.2%; Pred. No. 8.8e-09;
                                                                                                                                                                                                                                               PROTEIN-TYROSINE PHOSPHATASE.
                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                 BY SIMILARITY.
; 5112ADF290499139 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 IHKDMTLVDAIQQVAKNRCVL-PNRGFLKQLRELDKQLV 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       275 RINRVKLDEAFEFVKQRRSIISPNFSFMGGLLQFESOVL 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH-5).
DUSPB OR VH5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA.
                                                   Pfam; PF00782; DSPC; 1:
Pfam; PF00781; Rhodanese; 1.
SMART; SM00195; DSPC; 1.
SMART; SM00195; DSPC; 1.
SMART; SM00450; RHOD; 1.
PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50054; TYR_PHOSPHATASE_DAL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                        32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       625
DS_phosphatase.
Rhodanese_domain.
                InterPro; IPR001763; Rhodanese domain
InterPro; IPR000387; TYR_phosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE-Fetal brain;
MEDLINE-96009533; PubMed-7561881;
                                                                                                                                                                                                                                                                                           39541 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U27193; AAA83151.1; -.
                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 30.2 les 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                     Hydrolase, Cell cycle.
DOMAIN 175 367
ACT_SITE 258 258
SEQUENCE 367 AA; 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DUS8_HUMAN
                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D-----LPTFDLSVFFYPAAAFIDRA-LSDDHSKILVHCVMGRSRSATLVLAYLMIHKD 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 VNEVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDXYRDMDIQYHGVEAD 114
                                                                                                                                                                                                                                                              CH2 A DOMAIN.
CH2 B DOMAIN.
PROTEIN-TYROSINE PHOSPHATASE.
POLY-ARG.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              52; Indels
                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY.
416F429A12C1FA7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 163; DB 1;
Pred. No. 3.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168 MTLVDAIQQVAKNR-CVLPNRGFLKQLRELDKQL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |: || : | | : | 0.257 MSSDDAYRFVKDRRPSISPNFNFLGQLLEYERSL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                            31; Mismatches
                                                                                                                                                                                                       PROSITE; PS00383; TYR_PHOSPHATASE_1; 1. PROSITE; PS50056; TYR_PHOSPHATASE_2; 1. PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8, 2002, 15:45:16
                                                                                                                                                                                                                                                                                                                                     POLY-GLY.
POLY-SER.
PRO-RICH.
                                                                                                           MGD; MGI:106626; Nttpl.
InterPro; IPR000340; DS_phosphatase.
InterPro; IPR001763; Rhodanese_domain.
InterPro; IPR000387; TYR_phosphatase.
Pfam; PF00782; DSPC; 1.
SMART; SM00195; DSPC; 1.
SMART; SM00450; RHOD; 1.
                                                                                                                                                                                                                                                                                                                                                                                           ₹
                                                                                            EMBL; X95518; CAA64772.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                    14.0%;
31.8%;
                                                                                                                                                                                                                                                   Hydrolase; Nuclear protein.
DOMAIN 28 43
                                                                                                                                                                                                                                                                                                                                                                                          68847
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     completed: February
ne: 190 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    time:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search
Job tim
  qa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 VNEVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEAD 114
                                                                                                                                                                                                                                                                                                                                                                D-----LPTFDLSVFFYPAAAFIDRA-LSDDHSKILVHCVMGRSRSATLVLAYLMIHKD 167
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1999 (Rel. 38, Last sequence update)
C-AUG-2001 (Rel. 40, Last annotation update)
DUAL SPECIFICITY PROTEIN PHOSPHATASE 8 (EC 3.1.3.48) (EC 3.1.3.16)
(NEURONAL TYROSINE THREONINE PHOSPHATASE 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -:- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O = PROTEIN TYROSINE + PHOSPHATE.
-: SUBCELLULAR LOCATION: CYTOPLASMIC AND NUCLEAR.
-:- TISSUE SPECIFICITY: STRESSED PREDOMINANTLY IN BRAIN AND LUNG.
-:- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                        22;
                                                                                                                                                                                                                                                                                         14.0%; Score 163; DB 1; Length 625; 32.5%; Pred. No. 3.4e-08; tive 30; Mismatches 52; Indels
                                                                                                                                                                            CH2 A DOMAIN.
CH2 B DOMAIN.
PROTEIN-TYROSINE PHOSPHATASE.
PRO-RICH.
                                                                                                                                                                                                                                   BY SIMILARITY.
DCBEA14487219666 CRC64;
          InterPro: IPR000340; DS_phosphatase.
InterPro: IPR002965; P_rich_axtensn.
InterPro: IPR001763; Rhodanese_domain.
InterPro: IPR001387; TYR_phosphatase.
Pfam: PF00782; DSPC: 1.
PRINTS: PR00171; PRICHEXTENSN.
SWART; SW00195; DSPC: 1.
SWART; SW00195; DSPC: 1.
PROSITE; PS50056; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
PHOTOLASE: Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           663 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            168 MTLVDAIQQVAKNR-CVLPNRGFLKQLRELDKQL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1: || : | | : | | 267 MSSDDAYREVKDRRPSISPNFNFLGQLLEYERTL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 38, Created)
(Rel. 38, Last seq
                                                                                                                                                                                                                                                 65840 MW;
                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                625 AA;
                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DUSP8 OR NTTP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DUS8_MOUSE
                                                                                                                                                                                                                                   ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                               DOMAIN
                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                     115
                                                                                                                                                                                                                                                                                                                     Matches
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7

Gaps

22;

Length 663;

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 8, 2002, 15:40:56 ; Search time 15.19 Seconds
(without alignments)
1103.252 Million cell updates/sec Run on:

US-09-847-519A-2 1161 1 WYSGEVKTSLKNAYSSAKRL......VQQRRRSQRQDGEEEDGREL 220 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 Total number of hits satisfying chosen parameters:

219241 seqs, 76174552 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% . Listing first 45 summaries

PIR\_68:\* Database :

pirl:\* pir2:\* pir3:\* pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ecificity	u	_	specific				ein tyros	dual specificity p	protein tyrosine p	thetical	specific	dual specificity p	dual specificity p	probable protein p	protein tyrosine p	dual specificity p	hypothetical prote		S	hypothetical prote	hypothetical prote	probable dual spec	dual specificity p	phosphatase-like p	protein-tyrosine-p	dual specificity p	hypothetical prote	probable dual spec
SUMMARIES	ΩI	A47196	T32494	$\sim$	A56947	A56115	B57126	A57126	149365	S29090	149364	T21380	S24411	S52265	T03074	G84458	T39698	138890	T16056	T18915	T48906	T17802	T15969	S48459	S58725	T47666	S31304	QQVZH1	S41012	T30684
	DB	7	~	7	~	~	~	-	~	П	~	~	-	~	~	~	~	-	~	~	~	~	~	Н	-	~	Н	П	~	~
	Length	185	365	303	393	394	314	314	223	367	202	226	367	367	142	283	330	384	186	272	276	204	619	209	489	771	364	171	292	169
æ	Query	29.8	7	ė.	٠,	é.	٠	15.5	υ.	÷	14.5	ξ.	4	4	ω.		۳,	۳,		11.8					10.7					
	Score	346.5	204.5	192.5	192.5	192.5	184.5	180.5	174	169	168	168	166	166	160.5	159	158	157.5	150.5	137	136.5	134.5	132.5	132	124.5	124	122	113	111	110.5
	Result No.		7	m	7	Ŋ	9	7	<b>6</b> 0	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

dual specificity p	dual specificity p	probable dual spec J1L protein – vari	dual-specificity M	protein tyrosine p	protein-tyrosine-p	prenylated protein	hypothetical prote	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	conserved hypothet	protein-tyrosine-p	hypothetical prote
B47452 A42514	136845	T28322 B72161	T39517	T10278	B48148	JC5982	T19418	A48148	S56283	T42636	D83329	A56059	F84771
77	٦,	N (4	7	~	Н	~	~	-	~	~	7	7	7
171	171	171	278	1.60	1442	173	272	1445	551	1422	437	173	383
6.0	9.1	9.1	8.7	8.4	8.4	8.3	8.1	8.1	7.8	7.8	7.8	7.3	7.3
108	106	106	101.5	86	97.5	96.5	93.5	93.5	91	91	90	82	82
30 31	32	ი ო ა 4	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1 A47196 dual specificity phosphorotein phosphatase (EC 3.1.3) DUSP3 [validated] - human dual specificity phosphoprotein phosphatase vHR; vH1-related dual-specificity ph N;Alternate names: protein-tyrosine-phosphatase vHR; vH1-related dual-specificity ph C;Species: Homo sapiens (man) C;Date: 21-Sep-1993 #sequence_revision 01-Mar-1996 #text_change 15-Sep-2000 C;Date: 21-Sep-1993 #sequence_revision 01-Mar-1996 #text_change 15-Sep-2000 C;Date: 21-Sep-1993 #sequence_revision 01-Mari, T.; Aaronson, S.A.  B;Eshibashi, T.; Bottaro, D.P.; Chan, A.; Miki, T.; Aaronson, S.A. Proc; Machalase and Coning of a human dual-specificity phosphatase. A;Reference number: A47196; MuID:93101689
 A; Molecule type: mRNA A; Residues: 1-185 < 15H> A; Cross-references: GB:L05147; NID:g181839; PIDN:AAA35777.1; PID:g181840 A; Cross-references: GB:L05147; NID:g181839; PIDN:AAA35777.1; PID:g181840 A; Experimental source: fibroblasts A; Note: sequence extracted from NCBI backbone (NCBIN:120790, NCBIP:120791) (R; Denn, J. M; Zhou, G.; Mu, L.; Zhao, R.; Yuvaniyama, J.; Saper, M.A.; Dixon, J.E. (R; Denn, J.M; Zhou, G.; Wu, A1945, A1945)
Al Title: The purification and characterization of a human dual-specific protein tyro A; Title: The purification and characterization of a human dual-specific protein A; Reference number: A58760; MUID:95181338 A; Accession: A587760 A; Modecule type: protein A; Residues: 2.7 CDEN>
 Killy will yally and to the Brookhaven Protein Data Bank, February 1996 A; Reference number: A66852; PDB:1VHR A; Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 8-185 A; Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 8-185 B; Zhou, G.; Denu, J.M.; Wu, L.; Dixon, J.E. J. Biol. Chem. 269, 28084-28090, 1994 A; Title: The catalytic role of Cys(124) in the dual specificity phosphatase VHR. A; Reference number: A55447; MUID:95050584 A; Contents: annotation; active site
C;Genetics: A;Gene: GDB:DUSP3; VHR A;Cross-references: GDB:342110; OMIM:600183 A;Map Posttion: 17q21-17q21
 C; Function: catalyzes hydrolysis of peptidyl-phosphoserine, -phosphothreonine and C; Superfamily: dual specificity phosphoprotein phosphatase DUSP3; VH1-type dual spec C; Keywords: phosphototein; phosphotic monoester hydrolase C; Keywords: phosphototein; phosphatase phosphatase predicted <pre>KF:2-185/Product: dual specificity phosphatase</pre>

37 GAFE----LERLFWKGSPQYT----HVNEVWPKLYIGDEATALDRYRLQKAGFTHVLNA 87

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Ouery Match 29.8%; Score 346.5; DB 1; Best Local Similarity 43.8%; Pred. No. 1.2e-24; Matches 78; Conservative 35; Mismatches 54;

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Indels 11; Gaps

Length 185;

us-09-847-519a-2.rpr

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58;
      29; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 VAKNRCVL-PNRGFLKQLRELDKQLV 201
        Conservative
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A; Residues: 1-394 <GUA>
    50;
                                            57
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      Matches
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Superfamily: dual specificity phosphoprotein phosphatase 1; VH1-type dual specificity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:AF036685; PIDN:AAB88308.1; GSPDB:GN00022; CESP:C05B10.1 A;Experimental source: strain Bristol N2; clone C05B10 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
                                                                                                                                                                                                                                                                             hypothetical protein C05B10.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T34040
R;Gelsel, C.; Wamsley, P.
submitted to the RmL Data Library, December 1997
A;Description: The sequence of C. elegans cosmid C05B10.
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T46405
T46405
T46405
T6405
T6405
T6405
T6705
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 02-Sep-2000
C;Accession: T46405
R;Blum, H.; Bauersachs, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, January 2000
A;Reference number: 223034
                                                          88 AHGR--WNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILV 145
                                                                                    122 SVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAK-N 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 TKFFPEAISFIDDARRND-SACLVHCLAGISRSVTICLAYLMKTEMCTLDSAYEWVQKRN 301
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146 HCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQLVQQ 203
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A; Residues: 1-303 <AAA.
A; Cross-references: BMBL; AL137704
A; Experimental source: adult testis; clone DKF2p43401321
C; Genetics:
A; Note: DKF2p43401321.1
C; Superfamily; dual specificity phosphoprotein phosphata:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: CESP:CO5B10.1
A;Map position: 4
A;Introns: 22/2; 46/2; 74/3; 163/2; 204/2; 248/1; 287/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 204.5; DB 2;
; Pred. No. 3.4e-11;
24; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: T32494
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-365 <GEL>
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38.6%;
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Best Local Similarity 38.64
Matches 54; Conservative
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A; Status: preliminary
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Length 303

Score 192.5; DB 2; Pred. No. 3.4e-10;

16.6%; 34.2%;

Query Match Best Local Similarity

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C. Accession: A56947

R. Misra-Press, A.; Rin, C. S.; Yao, H.; Roberson, M.S.; Stork, P.J.S.

R. Misra-Press, A.; Rin, C. S.; Yao, H.; Roberson, M.S.; Stork, P.J.S.
J. Biol. Chem. 270, 14587-14596, 1995
A; Title: A novel mitogen-activated protein kinase phosphatase. Structure, expression A; Reference number: A56947
A; Reference number: A56947
A; Status: preliminary
A; Molecule type: mRNA
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-393 < MIS>
C; Superfamily: dual specificity phosphoprotein phosphatase 1; VH1-type dual specific C; Keywords: phosphoprotein; phosphoric monoester hydrolase
F; 202-333/Domain: VH1-type dual specificity phosphoprotein phosphatase homology <VH1
F; 2799/Active site: Cys (phosphocysteine intermediate) #status predicted
F; 285/Binding site: substrate phosphate (Arg) #status predicted
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R;Guan, K.L.; Butch, E.
R;Guan, K.L.; Butch, E.
A;Title: Isolation and characterization of a novel dual specific phosphatase, HVH2, A;Title: Isolation and characterization of a Novel dual specific phosphatase, HVH2, A;Title: Isolation and characterization of a novel dual specific phosphatase, HVH2, A;Title: Isolation and characterization of a novel dual specific phosphatase, HVH2, A;Accession: A56115; MUID:95221370
A;Accession: A56115
A;Status: preliminary; not compared with conceptual translation
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4
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N;Alternate names: mitogen-activated protein kinase phosphatase 2
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 17-Mar-1999
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                                                                                 EVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDL 116
                                                                                                                              117 PTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQ 176
                                                                                                                                                                                                                                                                                                          57 EVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDL 116
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Indels
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C,Genetics:
GGGene: GBB:DUSP4; HVH2; MKP-2
A,Cross-references: GDB:433893
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H.; Stebenlist,

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A Description: catalyzes the hydrolysis of peptidyl-phosphoserine, -phosphothreonine C; Superfamily: dual specificity phosphoprotein phosphatase 1; VH1-type dual specific C; Keywords: nucleus; phosphoprotein; phosphoric monoester hydrolase F; 140-160/Region: nucleus; pacation signal F; 180-311/Domain: VH1-type dual specificity phosphoprotein phosphatase homology <VH1 F; 257/Active site: Cys (phosphocysteine intermediate) #status predicted F; 263/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein tyrosine phosphatase - mouse (Species: Mus musculus (house mouse) (Species: Mus musculus (house mouse) (Species: Mus musculus (house mouse) (Spate: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999 (Spates) (Spa
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C;Superfamily: VH1-type dual specificity phosphoprotein phosphatase homology
F;36-174/Domain: VH1-type dual specificity phosphoprotein phosphatase homology
                                                                             Chacesion: A57126
Richan, P.J.; Davis, P.; Moskaluk, C.A.; Kearns, M.; Krutzsch, H.; Slebenlis Science 259, 1763-1766, 1939
A; Title: PAC-1: a mitogen-induced nuclear protein tyrosine phosphatase. A; Reference number: A57126; MUID: 93206122
A; Reference number: A57126; MUID: 93206122
A; Status: nucleic acid sequence not shown A; Status: nucleic acid sequence not shown A; Status: nucleic acid sequence not shown A; Status: nucleic acid sequence not shown A; Status: nucleic acid sequence not shown A; Status: nucleic acid sequence not shown A; Status: nucleic acid sequence sequence not shown A; Status: nucleic acid sequence not shown A; Map position: 2411-2411
                C;Species: Homo sapiens (man)
C;Date: 03-Nov-1995 #sequence_revision 02-Jul-1996 #text_change 11-Jun-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 PKMEEEGEEEDYCTPGAFELERLFWKGSPQYTHVNEVWPKLYIGDEATALDRYR--LQKA 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.0%; Score 174; DB 2; 30.2%; Pred. No. 1.2e-08; Live 31; Mismatches 68
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Best Local Similarity 32.2%
Matches 47; Conservative
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Matches 55; Conserv
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A57126
dual specificity phosphoprotein phosphatase (EC 3.1.3.-) 2 - human
N.Alternate names: mitogen-induced nuclear tyrosine phosphatase; phosphatase of activate
A;Map position: 8p21-8p11.2
(Superfamily: dual specificity phosphoprotein phosphatase 1; VH1-type dual specificity
C;Keywords: phosphoprotein; phosphoric monoester hydrolase
F;203-334/Domain: VH1-type dual specificity phosphorotein phosphatase homology <VH1>
F;280/Active site: Cys (phosphocysteine intermediate) #status predicted
F;286/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Accession: B57126
A.Status: preliminary
A.Molecule type: mRMA
A.Molecule type: mRMA
A.Residues: 1-314 <ROH>
A.Cross-references: GB:L11330
C.Superfamily: dual specificity phosphoprotein phosphatase 1; VH1-type dual specificit (C.Superfamily: vH1-type dual specificity phosphoprotein phosphatase hydrolase
F.180-311/Domain: VH1-type dual specificity phosphoprotein phosphatase homology <VH1>
F.257/Active site: Cys (phosphocysteine intermediate) #status predicted
F.263/Binding site: substrate phosphate (Arg) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dual specificity phosphatase (EC 3.1.3.-) 2 - mouse
N;Alternate names: mitogen-induced nuclear protein-tyrosine-phosphatase PAC-1
C;Specias: Mus musculus (house mouse)
C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 24-Apr-1998
C;Accession: B57126
R;Rohan, P.J.: Davis, P.; Moskaluk, C.A.; Kearns, M.; Krutzsch, H.; Siebenlist A;Title: PAC-1: a mitogen-induced nuclear protein tyrosine phosphatase.
A;Reference number: A57126; MUID:99200122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         198 EILPFLYLGSAYHAARRDMLDALGITALLNVS-----SDCPNHF-EGHYQYKCIPVEDH 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 PTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 LRGGFKSFQTYCPDLCSEAPAQALPPAGAENSNSDPRVPIYDQGGPV----EILPYLYL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVF 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 394;
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                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                         16.6%; Score 192.5; DB 2 34.2%; Pred. No. 4.8e-10; ive 29; Mismatches 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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310 VKQRRSIISPNFSFMGQLLQFESQVL 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177 VAKNRCVL-PNRGFLKQLRELDKQLV 201
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Best Local Similarity 28.33
Matches 56; Conservative
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                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 50; Conserv
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Gaps

6

<VH1;

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A;Cross-references: EMBL:U34973; NID:g1063624; PIDN:AAA87036.1; PID:g1063625
C;Superfamily: VHI-type dual specificity phosphoprotein phosphatase homology
F;36-174/Domain: VHI-type dual specificity phosphoprotein phosphatase homology <VHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dual specificity phosphoprotein phosphatase (EC 3.1.3.-) 1 - mouse N:Alternate names: 3CH134 protein; protein-tyrosine-phosphatase erp, nonreceptor typ
                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein F26A3.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Adte: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 15-0ct-1999
C;Adte: 15-0ct-1999 #sequence_revision 15-0ct-1999
R;McMurray, A.
Submitted to the EMBL Data Library, August 1996
A;Reference number: 219415
A;Reference number: 219415
A;Recession: T21380
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Reldues: 1-226 <WILD
A;Residues: 1-226 <WILD
A;Cross-references: EMBL: Z78419; PIDN: CABO1700.1; GSPDB: GN00019; CESP: F26A3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 GFTHVLNAAHGRWNVDTG---PDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAFIDRAL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 LFWKGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRD 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M-DIQYHGVEADDLPTFDLSVFFYPAAAFID----RALSDDHSKILVHCVMGRSRSATLVL 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 SDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNR-CVLPNRGFLKQLR 194
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                                                                                                                                                                                                                                                                                                                                        , 19
A;Reference number: 149364; MUID:96070766
A;Accession: 149364
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-205 <RES>
                                                                                                                                                                                                                                                                                 14.5%; Score 168; DB 2; 30.2%; Pred. No. 3.8e-08; iive 30; Mismatches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.5%; Score 168; DB 2; 30.8%; Pred. No. 4.3e-08;
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A:Introns: 117/2; 150/3; 186/3
                                                                                                                                                                                                                                                                                                          Best Local Similarity 30.2
Matches 54; Conservative
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Best Local Similarity
Matches 56; Conserv
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QL 171
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A; Accession: S29090
A; Molecule type: mRNA
A; Molecule type: martell, K.J.; Dixon, J.E.
B; Kwak, S.P.; Hakes, D.J.; Martell, K.J.; Dixon, J.E.
A; Biol. Chem. 269, 3596-3604, 1994
A; Title: Isolation and characterization of a human dual specificity protein-tyrosine phc
A; Reference number: A53052; MUID:94148864
A; Accession: A53052
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C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: 149364
R;Wishart, M.J.; Denu, J.M.; Williams, J.A.; Dixon, J.E.
J. Biol. Chem. 270, 26782-26785, 1995
A;Title: A single mutation converts a novel-phosphotyrosine binding domain into a dual-s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              induce a human gene encoding a protein-tyrosine
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A;Map position: 5934-5934
C;Superfamily: dual specificity phosphoprotein phosphatase 1; VH1-type dual specificity
C;Superfamily: dual specificity phosphoric monester hydrolase; stress-induced fF;181-312/Domain: VH1-type dual specificity phosphorein phosphorein phosphatese homology <VH1>F;258/Active site: Cys (phosphocysteine intermediate) #status predicted
F;264/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Note: sequence extracted from NCBI backbone (NCBIN:143800, NCBIN:143802, NCBIN:143804 C;Genetics:
                                                                                                                                                                                                                                                                                                                             RESULT 9
$29090
dual specificity phosphoprotein phosphatase (EC 3.1.3.-) 1 - human
N.Alternate names: protein-tyrosine-phosphatase (L100; protein-tyrosine-phosphatase,
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 25-Feb-1994 #sequence_revision 02-May-1994 #text_change 11-Jun-1999
C;Accession: S29090; A33052
R;Keyse, S. M.; Emslie, E.A.
Nature 359, 644-647, 1992
A;Title: Oxidative stress and heat shock induce a human gene encoding a protein-tyros
A;Reference number: $29090; MUID: 93024952
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             56 GITHIICI ---RONIEANPIKPNF--QOLFRYLVLDIADNPVENIIRFFPMTKEFIDGSL 110
                                                                                                                137 SDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNR-CVLPNRGFLKQLRE 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44 LFWKGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRD 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 MDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLM 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   164 IHKDMTLVDAIQQVAKNRCVL-PNRGFLKQLRELDKQLV 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 169; DB 1;
; Pred. No. 6.4e-08;
33; Mismatches 64.
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Matches 48; Conservative
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A; Residues: 1-367 < KWA>
                                                                                                                                                                                               196 LD 197
                                                                                                                                                                                                                                                   170 YE 171
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: 684488
R;Lin, X:, Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujil, C.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Vent, Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: T03074
R; Bahr, U.; Tidona, C.A.; Darai, G.
Virus Genes 15, 235-245, 1997
A; Title: The DNA sequence of Chilo iridescent virus between the genome coordinates (A; Reference number: 214834; MUID:98141693
A; Accession: T03074
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Roticus: Preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-142 < CABA>
A; Residues: 1-142 < CABA>
A; Residues: 1-182 < CABA>
A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - Chilo iridescent virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dual specificity phosphoprotein phosphatase homolog - Chilo iridescent virus
C;Species: Chilo iridescent virus
C;Date: 24-Mar=1999 #sequence_revision 24-Mar=1999 #text_change 08-Oct=1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 YSHLQKVTTLIHDSI-ENGNKVLVHCQAGISRSATVVIAYIMRSKRYSLQDAFNFVKKKR 115
                         44 LFWKGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRD 103
                                                                                                                                                                                                                   104 MDIQYHGVEADDLPTFDLSVFFYPAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLM 163
                                                                                                                                                                                                                                                                           62 LYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDL 121
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                                                                                  15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 142;
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31.1%; Pred. No. 3.8e-07;
ive 28; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               275 RTNRVKLDEAFEFVKQRRSIISPNFSFMGQLLQFESQVL
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116 SIIFPNAGFIKQLAQFERWL 135
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Best Local Similarity 31.1
Matches 51; Conservative
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Les 46; Conserv
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A; Residues: 1-283 <STO>
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A;Map position: 2
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Matches
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A;Reference number: S24411; MUID:92158357
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C;Superfamily: dual specificity phosphoprotein phosphatase 1; VH1-type dual specificity
C;Keywords: phosphoprotein; phosphoric monoester hydrolase
F;Reynords: VH1-type dual specificity phosphoprotein phosphatase homology <VH1>
F;258/Active site: Cys (phosphocysteine intermediate) #status predicted
F;264/Binding site: substrate phosphate (Arg) #status predicted
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N.Alternate_names: protein-tyrosine-phosphatase CL100; protein-tyrosine-phosphatase,
C;Species: Mus musculus (house mouse)
C;Date: 19-Feb-1994 #sequence_revision 02-May-1994 #text_change 11-Jun-1999
C;Accession: A54681; S2441
C;Accession: A54681; S2441
Mol. Cell. Biol. 13, 5195-5205, 1993
A;Title: Structure, mapping, and expression of erp, a growth factor-inducible gene A;Reference number: A54681; MUID:93360956
A;Reference number: A54681
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 22-Jun-1999
C;Accession: $52265
B;Muda, M.; Schlegel, W.; Arkinstall, S.
B;Muda, M.; Schlegel, M.; Arkinstall, S.
B;Muda, M.;Muda, 
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A;Molecule type: mRNA
A;Residues: 1-367 <CHA>
A;CENAS-references: EMBL:X61940; NID:g49735; PIDN:CAA43944.1; PID:g49736
C;Genetics:
A;Gene: erp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:S64851; NID:g409976; PIDN:AAB27882.1; PID:g409977 R;Charles, C.H.; Abler, A.S.; Lau, L.F. Oncogene 7, 187-190, 1992
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Best Local Similarity 30.29
Matches 48; Conservative
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Best Local Similarity 30.29
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Introns: 123/1; 172/1; 245/1
                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-367 <NOG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44
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8

Gaps

28;

Indels

5

Gaps

14;

Length 283;

26 EEGEEEDYCTPGAFELERLFWKGSPQYTHVNEVWPK-LYIGDEATALDRYRLQ 77	20 EEGEVCGVCGHCMPVSSDTVAPQQVHVSAFPSEILPEFLYLGSYDNASRSELLK 73	78 KAGFTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALS 137	74 TQGISRVLNTVPMCQNLYRN-SFTYHGLDNEKVLQFDDAIKFLDQC-E 119	138 DDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNR 181	120 KDKARVLVHCMSGKSRSPAVVVAYLMKRKGWRLAESHQWVKQRR 163	
26	20	78	74	138	120	
Qy	do.	οy	Dβ	Qy	qq	

Search completed: February 8, 2002, 15:44:07 Job time: 191 sec